FIGURE 1

PANEL A

PANEL B

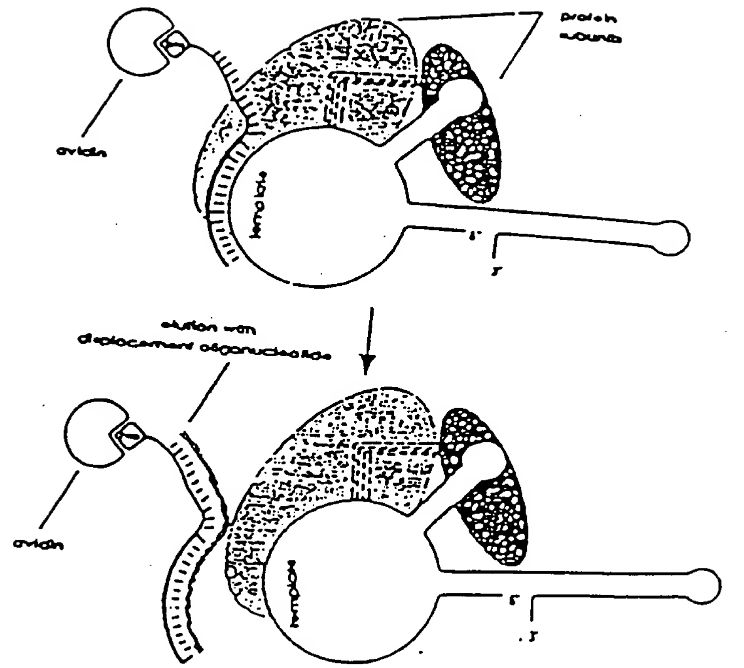


FIGURE 2

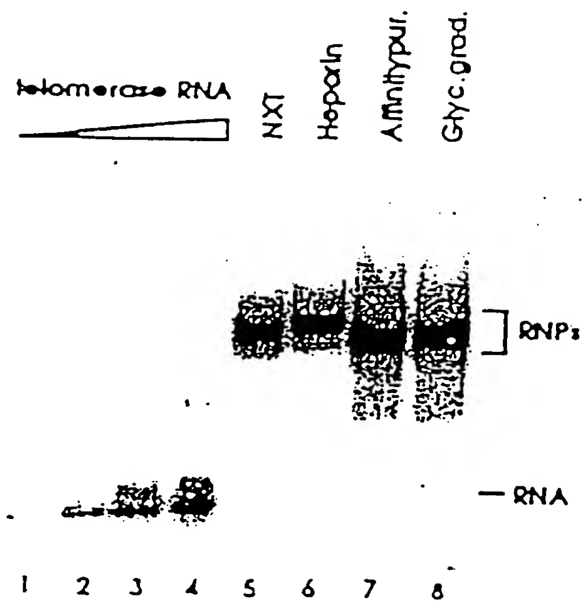
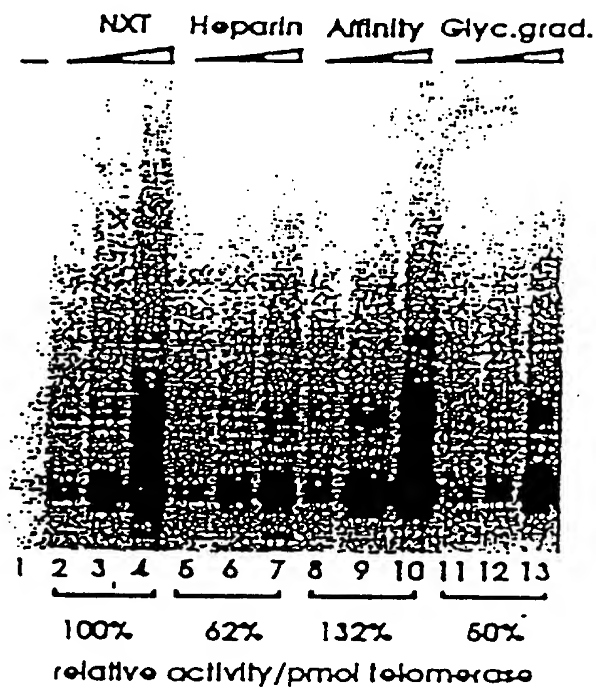
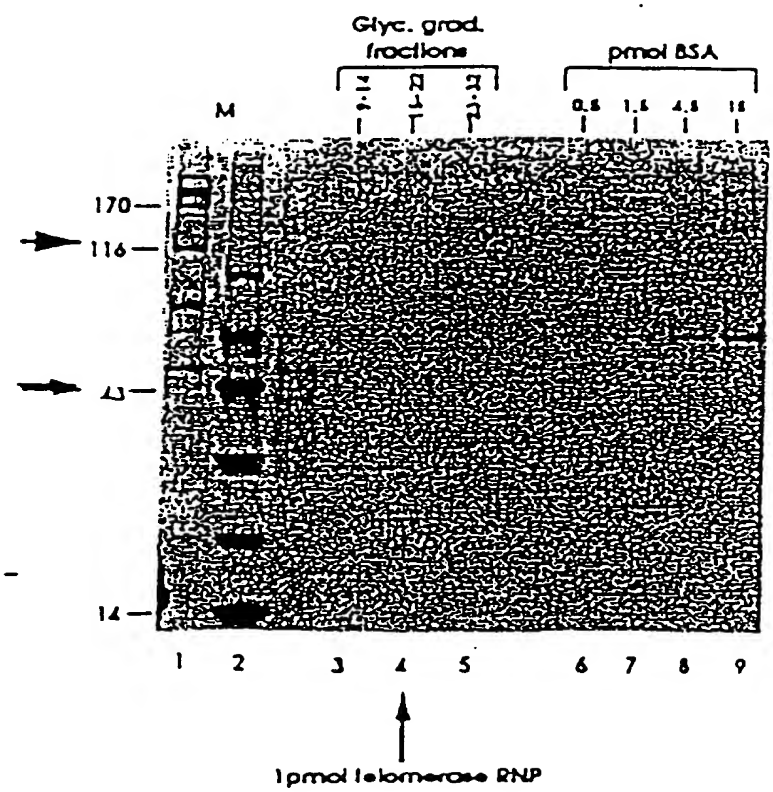

telomerase RNA
NXT
Heparin
Affinitypur.
Glyc.grad.
RNPs
RNA
1 2 3 4 5 6 7 8

FIGURE 3



NXT
Heparin
Affinity
Glyc.grad.
1 2 3 4 5 6 7 8 9 10 11 12 13
100%
62%
132%
60%
relative activity/pmol telomerase

FIGURE 4



Glyc. grad. fractions
pmol BSA
0.5
1.5
4.5
15
M
170
116
43
14
1
2
3
4
5
6
7
8
9
1pmol telomerase RNP

FIGURE 5

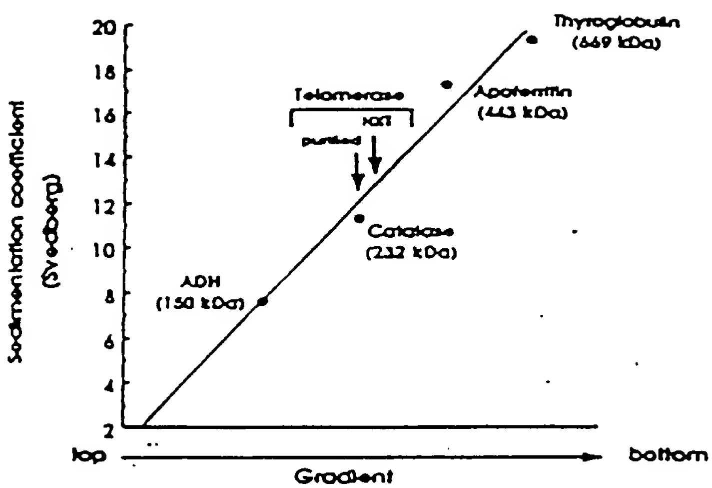

Sedimentation coefficient
(Svedberg)
20
18
16
14
12
10
8
6
4
2
Thyroglobulin
(669 kDa)
Apoferritin
(443 kDa)
Telomerase
purified
Catalase
(232 kDa)
ADH
(150 kDa)
top
bottom
Gradient

FIGURE 6

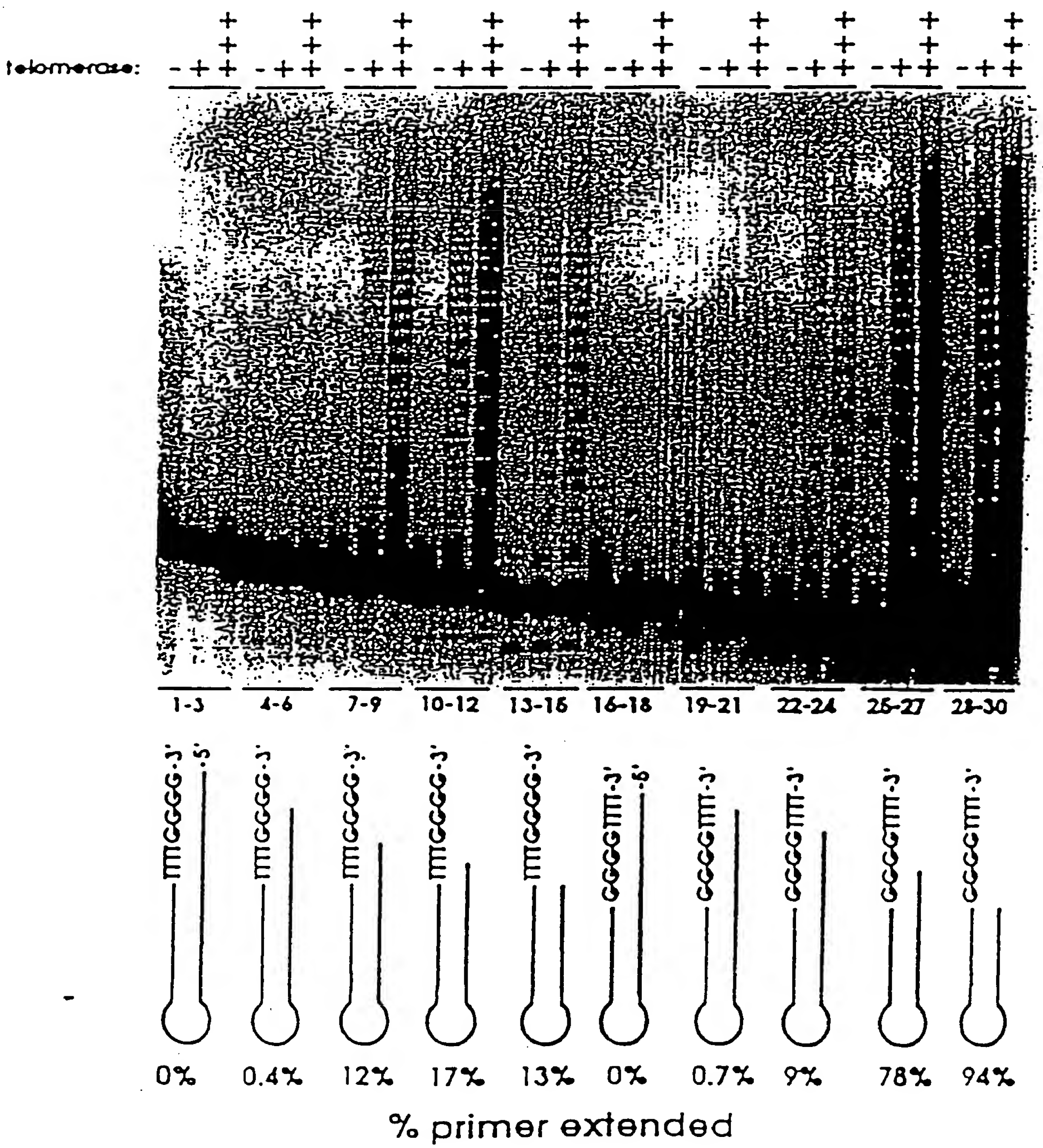
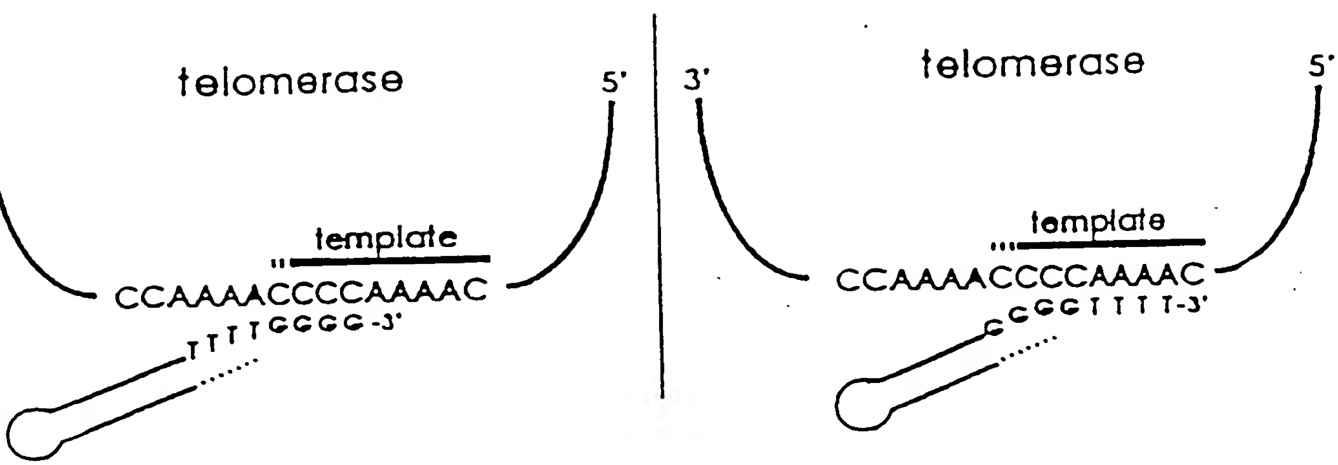

telomerase:
1-3
4-6
7-9
10-12
13-15
16-18
19-21
22-24
25-27
28-30
0%
0.4%
12%
17%
13%
0%
0.7%
9%
78%
94%
% primer extended

FIGURE 7



PANEL A

PANEL B

FIGURE 8

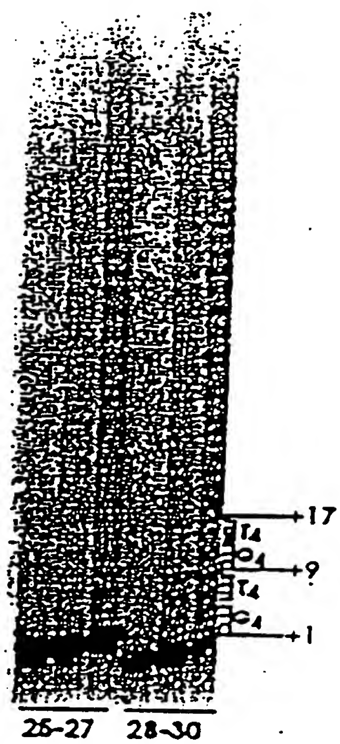


FIGURE 9

```
   1 AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT
  51 AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA
 101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCACTCAGC
 151 TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGA
 201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT
 251 TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG
 301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT
 351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAACTTCTT
 401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTCA
 451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCAA
 501 CTCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG
 551 ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA
 601 GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG
 651 ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA
 701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAT ACAATGTCAA
 751 GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAATA
 801 ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT TAATAGAAAT
 851 AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTC
 901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA
 951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG
1001 CTTGAGAAAG TCAAAGATTT TAACTTCAAC TACTATTTAA CAAAATCTTG
1051 TCCTCTTCCA GAAAATTGGC GGGAACGGAA ACAAAAAATC GAAAACTTGA
1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC
1151 TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTTCTA
1201 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC
1251 AAAAGAAAGT TAAGAAATAT GTGGAACTAA ACAAGCATGA ACTCATTCAC
1301 AAAAACTTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA
1351 GGTTGAGACC TCTGCAAAGC ATTTTTATTA TTTTGATCAC GAAAACATCT
1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGTCTCG
1451 CTGATTAGAT GATTTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA
1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA
1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT
1601 GAAGAATGGA AAAAGTCGCT TGGATTTGCA CCTGGAAAAC TCAGACTAAT
1651 ACCGAAGAAA ACTACTTTCC GTCCAATTAT GACTTTCAAT AAGAAGATTG
1701 TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC GAAGTTATTG
1751 AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC
1801 TTTTGGATTC GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG
1851 AGTTTGTTTG CAAATGGAAG CAAGTTGGAC AACCAAAACT CTTCTTTGCA
1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAACTATC
1951 AACATTCCTA AAAACTACTA AATTACTTTC TTCAGATTTC TGGATTATGA
2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC
2051 TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT
2101 TGCACTTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG
2151 AACAAAATGA CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA
2201 AGAAATTATT TTAAGAAAGA TAACTTACTT CAACCAGTCA TTAATATTTG
2251 CCAATATAAT TACATTAACT TTAATGGGAA GTTTTATAAA CAAACAAAAG
2301 GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTCATC ATTTTATTAT
```

FIGURE 10

1 MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNQSQSHYKD
51 LEDIKIFAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL
101 SSSDVSDRQK LQCFGFQLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM
151 IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGA
201 ADMNEPRCCS TCKYNVKNEK DHFLNNINVP NWNNMKSRTR IFYCTHFNRN
251 NQFFKKHEFV SNKNNISAMD RAQTIFTNIF RFNRIRKKLK DKVIEKIAYM
301 LEKVKDFNFN YYLTKSCPLP ENWRERKQKI ENLINKTREE KSKYYEELFS
351 YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHELIH
401 KNLLLEKINT REISWMQVET SAKHFYYFDH ENIYVLWKLL RWIFEDLVVS
451 LIRCFFYVTE QQKSYSKTYY YRKNIWDVIM KMSIADLKKE TLAEVQEKEV
501 EEWKKSLGFA PGKLRLIPKK TTFRPIMTFN KKIVNSDRKT TKLTTNTKLL
551 NSHLMLKTLK NRMFKDPFGF AVFNYDDVMK KYEEFVCKWK QVGQPKLFFA
601 TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNIVIDSKN
651 FRKKEMKDYF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKTLIVEAKQ
701 RNYFKKDNLL QPVINICQYN YINFNGKFYK QTKGIPQGLC VSSILSSFYY
751 ATLEESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVLFIEKL
801 INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI
851 SIDMKTLALM PNINLRIEGI LCTLNLNMQT KKASMWLKKK LKSFLMNNIT
901 HYFRKTITTE DFANKTLNKL FISGGYKYMQ CAKEYKDHFK KNLAMSSMID
951 LEVSKIIYSV TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFIEIFSTK
1001 KYIFNRVCMI LKAKEAKLKS DQCQSLIQYD A

FIGURE 11

1 CCCCAAAACC CCAAAACCCC AAAACCCCTA TAAAAAAAGA AAAAATTGAG
51 GTAGTTTAGA AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA
101 TTTGGATGAT ATAGAAAATT TACTTCCTAA TACATTCAAC AAGTATAGCA
151 GCTCTTGTAG TGACAAGAAA GGATGCAAAA CATTGAAATC TGGCTCGAAA
201 TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG AGTTCTACTT
251 CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTTAA
301 AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA
351 AATCAGGTAA TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA
401 TTATGGAGAA AATTACTTAA TACTAAAAGG TAAACAGTTT GGATTATTTC
451 CCTAGCCAAC AATGATGAGT ATATTAAATT CATATGAGAA TGAGTCAAAG
501 GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT AAAACGCAAG
551 AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTACTATTCG
601 TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC
651 TTGAGACAAT TGAAAAAGCT GTTTACAACT GAAGGAATCG CAGTTCTGAA
701 AGTTCTGATG TGTATGCCAT TATTTTGTGA ATTAATCTCA AATATCTTAT
751 CTCAATTTAA TGGATAGCTA TAGAAACAAA CCAAATAAAC CATGCAAGTT
801 TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC TGAATTTATA
851 TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC
901 TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT
951 AAAAGAAGCA GGCGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAAT
1001 TTGTTGATTC TTCTGTAACC GGAATTAACA ACAAGAATAT TAGCAACGAA
1051 AAAGAAGAAG AGCTATCACA ATCCTGATTC TTAAAGATTT CAAAAATTCC
1101 AGGTAAGAGA GATACATTCA TTAAAATTCA TATATTATAG TTTTTCATTT
1151 CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA
1201 GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT
1251 TCACATTCAT AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA
1301 GCAGTCATCC GTTTTAAAAA TAGTGCTATG AGGACTAAAT TTTTAGAGTC
1351 AAGAAATGGA GCCGAAATCT TAATCAAAAA GAATTGCGTC GATATTGCAA
1401 AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA ATCTTGATTG
1451 ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATTA AAGAAATAAA
1501 GTAACTTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG
1551 CGATCTTCAA TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA
1601 ATACAAACCT TGGTCAAAAT ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA
1651 AAAGAAAAAA TAAGGCAATA AATAAAATGA GTACAGAAGT GAAGAAATAA
1701 AAGATTTATT TTTTTCAATA ATTTATTGAA AAGAGGGGTT TTGGGGTTTT
1751 GGGGTTTTGG GG

FIGURE 12

```
    1  CCCCAAAACCCCAAAACCCCAAAACCCCTATAAAAAAAGAAAAAATTGAGGTAGTTTAGA
       ------------------------------------------------------------  60
       GGGGTTTTGGGGTTTTGGGGTTTTGGGGATATTTTTTTCTTTTTTAACTCCATCAAATCT

a      P  Q  N  P  K  T  P  K  P  L  ·  K  K  K  K  L  R  ·  F  R  -
b       P  K  T  P  K  P  Q  N  P  Y  K  K  R  K  N  C  G  S  L  E  -
c        P  K  P  Q  N  P  K  T  P  I  K  K  E  K  I  E  V  V  ·  K -

   61  AATAAAATATTATTCCCCGCACAAATGGAGATGGATATTGATTTGGATGATATAGAAAATT
       ------------------------------------------------------------  120
       TTATTTTATAATAAGGGGCGTGTTTACCTCTACCTATAACTAAACCTACTATATCTTTTAA

a      N  K  I  L  F  P  H  K  W  R  W  I  L  I  W  H  I  ·  K  I  -
b       I  K  Y  Y  S  R  T  N  G  D  G  Y  C  F  G  C  Y  R  K  F  -
c        ·  N  I  I  P  A  Q  H  E  H  D  I  D  L  D  D  I  E  N  L -

  121  TACTTCCTAATACATTCAACAAGTATAGCAGCTCTTGTAGTGACAAGAAAGGATGCAAAA
       ------------------------------------------------------------  180
       ATGAAGGATTATGTAAGTTGTTCATATCGTCGAGAACATCACTGTTCTTTCCTACGTTTT

a      Y  F  L  I  H  S  T  S  I  A  A  L  V  V  T  R  K  D  A  K  -
b       T  S  ·  Y  I  Q  Q  V  ·  Q  L  L  ·  ·  Q  E  R  M  Q  N  -
c        L  P  N  T  F  N  K  Y  S  S  S  C  S  D  K  K  G  C  K  T -

  181  CATTGAAATCTCGGCTCGAAATCGCCTTCATTGACTATTCCAAAGTTGCAAAAACAATTAG
       ------------------------------------------------------------  240
       GTAACTTTAGACCGAGCTTTAGCGGAAGTAACTGATAAGGTTTCAACGTTTTTGTTAATC

a      H  C  N  L  A  R  N  R  L  H  C  L  F  Q  S  C  K  N  N  ·  -
b       I  E  I  W  L  E  I  A  F  I  D  Y  S  K  V  A  K  T  I  R  -
c        L  K  S  G  S  K  S  P  S  L  T  I  P  K  L  Q  K  Q  L  E -

  241  AGTTCTACTTCTCGGATGCAAATCTTTATAACGATTCTTTCTTGAGAAAATTAGTTTTAA
       ------------------------------------------------------------  300
       TCAAGATGAAGAGCCTACGTTTAGAAATATTGCTAAGAAAGAACTCTTTTAATCAAAATT

a      S  S  T  S  R  H  Q  I  F  I  T  I  L  S  C  E  N  ·  F  ·  -
b       V  L  L  L  G  C  K  S  L  ·  R  F  F  L  E  K  I  S  F  K  -
c        F  Y  F  S  D  A  N  L  Y  N  D  S  F  L  R  K  L  V  L  K -

  301  AAAGCCGAGAGCAAAGAGTAGAAATTGAAACATTACTAATGTTTAAATAAAATCAGGTAA
       ------------------------------------------------------------  360
       TTTCGGCTCTCGTTTCTCATCTTTAACTTTGTAATGATTACAAATTTATTTTAGTCCATT

a      K  A  E  S  K  E  ·  K  L  K  H  Y  ·  C  L  N  K  I  R  ·  -
b       K  R  R  A  K  S  R  N  C  N  I  T  N  V  ·  I  K  S  G  N  -
c        S  G  E  Q  R  V  E  I  E  T  L  L  H  F  K  ·  N  Q  V  M -

  361  TGAGGATTATTCTATTTTTTAGATCACTTCTTAAGGAGCATTATGGAGAAAATTACTTAA
       ------------------------------------------------------------  420
       ACTCCTAATAAGATAAAAAATCTAGTGAAGAATTCCTCGTAATACCTCTTTTAATGAATT

a      C  G  L  F  Y  F  L  D  H  F  L  R  S  I  H  E  K  I  T  ·  -
b       E  D  Y  S  I  F  ·  I  T  S  ·  G  A  L  W  R  K  L  L  N  -
c        R  I  I  L  F  F  R  S  L  L  K  E  H  Y  G  E  N  Y  L  I -

  421  TACTAAAAGGTAAACAGTTTGGATTATTTCCCTAGCCAACAATGATGAGTATATTAAATT
       ------------------------------------------------------------  480
       ATGATTTTCCATTTGTCAAACCTAATAAAGGGATCGGTTCTTACTACTCATATAATTTAA

a      Y  ·  K  V  N  S  L  D  Y  F  P  S  Q  Q  C  C  V  Y  ·  I  -
b       T  K  R  ·  T  V  W  I  I  S  L  A  N  N  D  E  Y  I  K  F  -
c        L  K  G  K  Q  F  G  L  F  P  ·  P  T  M  M  S  I  L  N  S -
```

FIGURE 13

```
  2 EVDVDMQAQNHGIHSALKTCEEIKEAKTLYSWIQKVIRCRNQSQSHYKDL  51
    |::.  ; ::::|·  :|      |.::|      ::.  .  |  |..|.|.|
 19 ELELEMQENQNDIQVRVK....IDDPKQY..LVNVTAACLLQEGSYYQDK  62

 52 EDIKIFAQTNIVATPRDYNEEDFKVIARKEVF.STGLMIELIDKCLVELL 100
    ::     . ::    : .|.| ..|.. .|: ..:| |   ....::|.:
 63 DERRYIITKALL ...EVAESDPEFICQLAVYIRNELYIRTTTNYIVAF. 107

101 SSSDVSDRQKLQCFGFQLKGNQLAKTHLLTALSTQKQYFFQDEWNQVRAM 150
                ..: ....: ....: .|:  ..:.:   |:.||  :
108 .              CVVHKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYI 144

151 IGNELFRHLYTKYLIFQRTSEGTLVQFCGNNVFDHLKVNDKFDKKQKGGA 200
    ::.  ! :||                |  .: :.:: ..|.... ::: ::
145 FDATEFKNLY       ........LDRILSQDIRKELTFRKCLQRCVRSKF 181

201 ADMNE    PRCCSTCKYNVKNEKDHFLNNINVPNWNNMKSRTRIFYCTHF 247
    .::|:    ::|. :   . |... ::|. .|  ..|:. |.:
182 SEFNEYQLCKYCTES..QRKKTMFRYLSVTNKQKWDQTKKK..  ...  220

248 NRNNQFFKKHEFVSNKNNISAMDRAQTIFTNIFRFNRIRKKLKDKVIEKI 297
     |.: ...| : ·.:.:: | .: :          :|:..:   | ||. |:.||
221 .RKENLLTKLQAIKESEDKSKRETG.....DIMNVEDAIKALKPAVMKKI 264

298 AYMLEKVKDFNFNYYLTKSCPLPENWRERKQKIENLINKTREEKSKYYEE 347
    | .   :|                         :. | ..: |.| |.|   :.:
265 AKRQNAMK....  .....  .......KHMKAPKIPNSTLESKYLTFKD 294

348 LFSYTTDNKCVTQFINEFFYNILPKDFLTGRNRKNFQKKVKKYVELNKHE 397
    |:...  .  .      .| .|.||.|.:  .. :  .  .    . ..:| .|
295 LIKFCHISEP.    ..KERVYKILGKKYPKTEEEYKAAFGDSASAPFN.PE 338

398 LIHKNLLLEKINTREISWMQVETSAKHFYYFDHENIYVLWKLLRWIFEDL 447
    |  |.. :|   .|:| .: . :..|. :   :  .| ...  :|| : :
339 LAGKRMKIEISKTWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSN.. 386

448 VVSLIRCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSIADLKKETLAEVQE 497
                                   |:| ::.|
387                    ....  ..........ILKAGVSD........... 394

498 KEVEEWKKSLGFAPGKLRLIPKKTTFRPIMTFNKKIVNSDRKTTKLTTNT 547
                                                   ||:.
395                     .    ....................TTHS 398

548 KLLNSHLMLKTLKNRMFKDPFGFAVFNYDDVMKKYEEFVCKWKQVGQPKL 597
       !                                  :|. |.|:..|:
399 IVINK               .        .    .....  ....ICEPKAVENSKM 415

598 FFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKNNIVID 647
    |    :: ....: || | :.. :|..|     .:    :.:||   |:  |::
416 F  PLQFFSAIEAVN.EAVTKGFKAKK...RENMNLKGQIEAVKE..VVE 457

648 SKNFRKKEMKDYFRQKFQKIALEGGQYPTLFSVLENEQNDLNAKKTLIVE 697
    ..:   ||:|          .||..:  ..:..| |. ..:. .. .| :.
458 KTDEEKKDM...  .......ELEQTEEGEFVKVNEGIGKQYINSIELAIK 496

698 AKQRNYFKKDNLLQPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSS 747
       .. :..  .   :::.  .   .   :    |.   ::.  .|  .. :|:
497 IAVNKNLDEIKGHTAIFSDVSGSMSTSMSGGAKKYGSVRTCLECALVLGL 546

748 FYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLITTQENNAVLFI 797
    :  .  |.||: ::...| ..:.. ::: :
547 MVKQRCEKSSFYIFSSPSSQCNKCYLEVDL.................... 576

798 EKLINVSRENGFKFNMKK.LQTSFPLSPSKFAKYGMDSVEEQNIVQDYCD 846
           .::::: .|.| ||.. .|:.:   ..:. ::::|  .   ....|
577 ...   .  PGDELRPSMQKLLQEKGKLGGG..TDFPYECIDEWTKNKTHVD 617

847 WIGISIDMKTLALMPNINLRIEGILCTLNLNMQTKKASMWLKKKLKSFLM 896
    |.|  ||..  .  .:||:| .:|: .:                 ||.|.  :
618 NIVILSDMMIAEGYSDINVRGSSIVNSI...........  .KKYKDEVN 653

897 NNITHYFRKTITTEDFANKTLNKLFISGGYKYMQCAKEYKD.HFKKNLAM 945
    ||. :   .:. |:::                |::. :.|:.: :: | ::|
654 PNIKIF...AVDLEGYG...   ........KCLNLGDEFNENNYIKIFCM 687

946 SSMIDLEVSKIIYSVTRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHFIE 995
    |. |                  :|:: ..   :.               :::|
688 SDSI...............LKFISAKQGGA............  ..NMVE 706

996 IFSTKKYIFNRVC 1008
    ::   |.: :.::.
707 VI..KNFALQKIG 717
```

FIGURE 14

```
132  LSTQKQYFFQDEWNQVRAHIGNEL.FRHLYTKYLIFQRTSE..CTLVQFC  178
     :|  ..|          ....| ||||  :  :. .. :::.  |   |  | .
  1  MSRRNQ.   ....KKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQQI   43

179  CNNVFDHLKVNDKFDKKQKCCAADHNEPRCCSTCKYNVKNEKDHFLNNIN  228
     :: :. ||.::  :. ..|...| :|            | .|..::|..:|
 44  KEEDLKLLKFKNQDQDGNSGNDDDDEE.........NNSNKQQELLRRVN   84

229  VPNWNNHKSRTRIFYCTHFNRNNQFFKKHEFVSNKNNISAHDRAQTIFTN  278
                     ::... |::||   |:.| :  .   ..:.  .|
 85  ...          ......QIKQQVQLIKK...VGSKVEKDLNLNEDENKKN  114

279  IFRFNRIRKKLKDKVIEKIAYHLEKVKDFNFNYYLTKSCPLPENWRERKQ  328
     :. ..::..     ...|.  .     : | :::::.. |..|.. . ::|| .
115  GLSEQQVKEEQLRTITEEQVKYQNLVFNHDYQLDLNESGGHRRHRRETDY  164

329  KIENLINKTREEKSKYYEELFSYTTDNKCVTQFINE.FFYNILPKDFLTC  377
     ..|.::: .:::|                  .:|. : |:    |  : ||::.
165  DTEKWFEISHDQK...............NYVSIYANQKTSYCWWLKDYFNK  200

378  RNRKNFQKKVKKYVELNKHELIHKNLLLEKINTREISWHQVETSAKHFYY  427
     .|  .::.·.:.:.     .. |:.  : : :.|.   : |:  |:..
201  NNYDHLNVSINRLE..TEAEFYAFDDFSQTIKLTNNSYQTVNID......  242

428  FDHENIYVLWKLLRWI..FEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNI  475
     .: :| ..:: |||::  :| : :   ||: :   | .| .:.|.    ..|
243  VNFDNNLCILALLRFLLSLERFNILNIRSSY..TRNQYNFEKIGELLETI  290

476  WDVIHKHSIADLKKETLAEVQEKEVEEWKKSLGFAPGKLRLIPKKTTFRP  525
     :.|::.  .            .:|: .::   ..:.:  ...  .  |. |..
291  FAVVFSHR..          ..HLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQ  330

526  IHTFNKKIVNSDRKTTKLTTNTKLLNSHLHLKTLKNRHFKDPFGFAVFNY  575
     : .|...:     |   |.|:  .   |:|..  .|. :...  :.  .  || |.
331  VYSFSTDLKLVD..TNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENL  378

576  DDVHKKYEEFVCKWKQVGQPKLF.   .....FATHDIEKCYDS..VNREK  615
     : ::||          :.  |: |. |     :.  :.:| ..:.   :.::|
379  NVLLKKVKH    ANLNLVSIPTQFNFDFYFVNLQHLKLEFGLEPNILTKQK  426

516  LSTFL.        KTTKLLSSDFWIHTAQILKRKNNI..VIDSKNFRKKEHK  657
     |..:|         |. |:|  :|:. .||   .||. :   ... ||::....  .
427  LENLLLSIKQSKNLKFLRLNFYTYVAQETSRKQILKQATTIKNLKNNKNQ  476

558  DYFRQKFQKIALEGGQYPTLFSVLEN  EQNDLNAKKTLIVEAKQRNYFK  705
     :  . .            ::      |   |     | :|:...    ::|.|  |  .
477  EETPETKDETPSESTSGHKFFDHLSELTELEDFSVN..  .LQATQEIY   520

706  KDNELQPVIN:CQYNYINFNGKFYKQTKGIPQGLCVSSILSSFYYATLEE  755
      | |      |              .|  .. .  :.   :  ...|    |.||:
521  .DSLHKLLIRSTNLKKFKLSYKYEHEKSKHDTFIDLKNI..  ..YETLNN  564

756  SSLCFLADESMNPENPNVNLLHRLTDDYLLITTQENNAVLFIEKLINVSR  805
            |·  i : .||: i     ||:              .:..::  ||.
565  .     .LKRCSWNISNPHGNISYELTN      ......KDSTFYKFKLTLNQE  500

806  ENCFKFNHKKLQTSFPLSPSKFAKYCHDSVEEQNIVQDYCDWIGISIDHK  855
      .  |·.:|  !..|.:.   | ||.:  .|:|.  :  ::..|..|:  :  ::.
501  LQHAKYTFK   QNEFQFNNVKSAKIESSSLESLEDIDSLCKSIASCKNLQ  648

856  TLALHPNINLRIEGILCTLNLNHQT. KKASHWLKK..KLKSFLHNNITH  901
     .:..           | ·:|:. |:....   |..  :::|.   .||.:    .|.
649  NVNI.          IASLLYPNNIQKNPFNKPNLLFFKQFEQLKNLENVSINC  691

902  YFRKTI  . TTEDFANKTLNKLFISCGYKYHQCAKEYKDHFKKNLAHSSH  948
     :   |      |   .  .  | ||   |  .:|:   :|..  ||.    .:..:
692  ILDQHILNSISEFLEKNKKIKAFILKRYYLLQYYLDYTKLFKTLQQLPEL  741

→949  IDLEVSKIIYSVT                    .RAFFKYLVCNIKDT.  IFGEEHY  982
      :: :  .      |                   :||:. |.  ||:.  .:.  .:
742  NQVYINQQLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDF  791

983  PQFFLS  TLKHFIEIFSTKKY  IFNRVCHILKAKEAKLKSDQCQSLIQ  1028
     .   ·|     i   | ·|..i|     !·      ...    |  ..::.|.|:.
792  DQNTVSDDSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQELLK  840
```

FIGURE 15

```
  4  QIQLDDIENLLPNTFNKYSSSCSDKKGCKTLKSGSKSPSLTIPK......  47
     ::.  ..||.      ::::...| |..   :||.|....   :|| .|.
617  NVKSAKIESSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNP  666

 48            LQKQLEFYFSDANLYNDSFLRKLVLKSGEQRVE....IETLLM  86
                 ||:|  .  . .|:   :::|    :|.| .: :|     |..:::
667  FNKPNLLFFKQFEQLKNLENVSINCILDQHILNSISEFLEKNKKIKAFIL  716
```

FIGURE 16

```
  1 MEMDIDLDDIENL....LPNTFNKYSSSCSDKKGCKTLKSGSKSPS..  42
    :  |.      ||      ...|.. |:| |....:. . | || ..:
491 IELAIKIAVNKNLDEIKGHTAIFSDVSGSHSTSHSGGAKKYGSVRTCLEC 540

 43  LTIPKLQKQ......LEFYFSDANLYNDSFLRKLVLKSGEQRVEIETLL  85
     |.:   : ||      : :: |... :|.::| .: |.::| |..::.||
541 ALVLGLMVKQRCEKSSFYIFSSPSSQCNKCYL.EVDLPGDELRPSMQKLL 589
```

FIGURE 17

```
                          Motif A                                      Motif B
Consensus                h--hDh---h--h                               h---+-QG---SP
telomerase p123 GQPKLFFATMDIEKCYDSVNREKLSTFLKTTKLL-100-KFYKQTKGIPQGLCVSSILSSFYYATLEESSLGPL
Dong (LINE)     KNRNLHCTYIDYKKAFDSIPHSWLIQVLEIYKIN- 28-RQIAIKKGIYQGDSLSPLWFCLALNPLSHQLHNDR
al S.c.(groupII)FGGSNWFREVDLKKCFDTISHDLIIKELKRYISD- 26-HVPVGPRVCVQGAPTSPALCNAVLLRLDRRLAGLA
HIV-RT          LKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIP-  7-GIRYQYNVLPQGWKGSPAIFQSSMTKILEPFRKQN
L8543.12 YAAH   VLPELYFMKFDVKSCYDSIPRMECMRILKDALKN- 68-RCYIREDGLFQGSSLSAPIVDLVYDDLLEFYSEPK

                        Motif C                           Motif D           Motif E
Consensus              h--YhDDhhh                        Gh-h---K           h-hLGh-h
telomerase p123 -14-LMRLTDDYLLITTQENN-0-AVLFIEKLINVSRENGFKFNMKKLQT-23-QDYCDWIGISI
Dong (LINE)     -16-HLIYMDDIKLYAKNDKE-0-MKKLIDTTTIFSNDISMQFGLDKCKT-25-KCLYKYLGFQQ
al S.c.(groupII)-55-YVRYADDILIGVLGSKN-2-KIIKRDLNNFLNS.LGLTINEEKTLI- 4-ETPARFLGYNI
HIV-RT          - 4-IYQYMDDLYVGSHLEIG-1-HRTKIEELRQHLLRWGLTTPDKKHQK- 0-EPPFLWMGYEL
L8543.12 YAAH   - 8-ILKLADDFLIISTDQQQ........VINIKKLAMGFQKYNAKANR-41-IRSKSSKGIFR
```

FIGURE 18

```
telomerase p43    LQKQLEFYFSDANLYNDSFLRKLVLKSGEQRVEIETLLM
human La          ICHQLEYYFGDFNLPRDKFLKEQI.KLDEGWVPLEIMIK
Xenopus LaA       ICEQIEYYFGDHNLPRDKFLKQQI.LLDDGWVPLETMIK
Drosophila La     ILRQVEYYFGDANLNRDKFLREQIGKNEDGWVPLSVLVT
S. c. Lhp1p       CLKQMEFYFSEFNFPYDRFLRTTAEK.NDGWVPISTIAT
```

FIGURE 19

1 aactcattta attactaatt taatcaacaa gattgataaa aagcagtaaa taaaacccaa
61 tagatttaat ttagaaagta tcaattgaaa aatggaaatt gaaaacaact aagcacaata
121 gccaaaagcc gaaaaattgt ggtgggaact tgaattagag atgcaagaaa accaaaatga
181 tatataagtt agggttaaga ttgacgatcc taagcaatat ctcgtgaacg tcactgcagc
241 atgtttgttg taggaaggta gttactacta agataaagat gaaagaagat atatcatcac
301 taaagcactt cttgaggtgg ctgagtctga tcctgagttc atctgctagt tggcagtcta
361 catccgtaat gaactttaca tcagaactac cactaactac attgtagcat tttgtgttgt
421 ccacaagaat actcaaccat tcatcgaaaa gtacttcaac aaagcagtac ttttgcctaa
481 tgacttactg gaagtctgtg aatttgcata ggttctctat atttttgatg caactgaatt
541 caaaaatttg tatcttgata ggatactttc ataagatatt cgtaaggaac tcactttccg
601 taagtgttta caaagatgcg tcagaagcaa gttttctgaa ttcaacgaat actaacttgg
661 taagtattgc actgaatcct aacgtaagaa aacaatgttc cgttacctct cagttaccaa
721 caagtaaaag tgggattaaa ctaagaagaa gagaaaagag aatctcttaa ccaaacttta
781 ggcaataaag gaatctgaag ataagtccaa gagagaaact ggagacataa tgaacgttga
841 agatgcaatc aaggctttaa aaccagcagt tatgaagaaa atagccaaga gatagaatgc
901 catgaagaaa cacatgaagg cacctaaaat tcctaactct accttggaat caaagtactt
961 gaccttcaag gatctcatta agttctgcca tatttctgag cctaaagaaa gagtctataa
1021 gatccttggt aaaaaatacc ctaagaccga agaggaatac aaagcagcct ttggtgattc
1081 tgcatctgca cccttcaatc ctgaattggc tggaaagcgt atgaagattg aaatctctaa
1141 aacatgggaa aatgaactca gtgcaaaagg caacactgct gaggtttggg ataatttaat
1201 ttcaagcaat taactcccat atatggccat gttacgtaac ttgtctaaca tcttaaaagc
1261 cggtgtttca gatactacac actctattgt gatcaacaag atttgtgagc ccaaggccgt
1321 tgagaactcc aagatgttcc ctcttcaatt ctttagtgcc attgaagctg ttaatgaagc
1381 agttactaag ggattcaagg ccaagaagag agaaaatatg aatcttaaag gtcaaatcga
1441 agcagtaaag gaagttgttg aaaaaaccga tgaagagaag aaagatatgg agttggagta
1501 aaccgaagaa ggagaatttg ttaaagtcaa cgaaggaatt ggcaagcaat acattaactc
1561 cattgaactt gcaatcaaga tagcagttaa caagaattta gatgaaatca aaggacacac
1621 tgcaatcttc tctgatgttt ctggttctat gagtacctca atgtcaggtg gagccaagaa
1681 gtatggttcc gttcgtactt gtctcgagtg tgcattagtc cttggtttga tggtaaaata
1741 acgttgtgaa aagtcctcat tctacatctt cagttcacct agttctcaat gcaataagtg
1801 ttacttagaa gttgatctcc ctggagacga actccgtcct tctatgtaaa aacttttgca
1861 agagaaagga aaacttggtg gtggtactga tttcccctat gagtgcattg atgaatggac
1921 aaagaataaa actcacgtag acaatatcgt tattttgtct gatatgatga ttgcagaagg
1981 atattcagat atcaatgtta gaggcagttc cattgttaac agcatcaaaa agtacaagga
2041 tgaagtaaat cctaacatta aaatctttgc agttgactta gaaggttacg gaaagtgcct
2101 taatctaggt gatgagttca atgaaaacaa ctacatcaag atattcggta tgagcgattc
2161 aatcttaaag ttcatttcag ccaagcaagg aggagcaaat atggtcgaag ttatcaaaaa
2221 ctttgccctt caaaaaatag gacaaaagtg agtttcttga gattcttcta taacaaaaat
2281 ctcaccccac ttttttgttt tattgcatag ccattatgaa atttaaatta ttatctattt
2341 atttaagtta cttacatagt ttatgtatcg cagtctatta gcctattcaa atgattctgc
2401 aaagaacaaa aaagattaaa a

FIGURE 20

MEIENNQAQQPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL

VNVTAACLLQEGSYYQDKDERRYIITKALLEVAESDPEFICQLAVYIRNELYIRTTTN

YIVAFCVVHKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYIFDATEFKNLYLDRILS

QDIRKELTFRKCLQRCVRSKFSEFNEYQLGKYCTESQRKKTMFRYLSVTNKQKWDQTK

KKRKENLLTKLQAIKESEDKSKRETGDIMNVEDAIKALKPAVMKKIAKRQNAMKKHMK

APKIPNSTLESKYLTFKDLIKFCHISEPKERVYKILGKKYPKTEEEYKAAFGDSASAP

FNPELAGKRMKIEISKTWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSNILKAGV

SDTTHSIVINKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKRENMNLKGQIE

AVKEVVEKTDEEKKDMELEQTEEGEFVKVNEGIGKQYINSIELAIKIAVNKNLDEIKG

HTAIFSDVSGSMSTSMSGGAKKYGSVRTCLECALVLGLMVKQRCEKSSFYIFSSPSSQ

CNKCYLEVDLPGDELRPSMQKLLQEKGKLGGGTDFPYECIDEWTKNKTHVDNIVILSD

MMIAEGYSDINVRGSSIVNSIKKYKDEVNPNIKIFAVDLEGYGKCLNLGDEFNENNYI

KIFGMSDSILKFISAKQGGANMVEVIKNFALQKIGQK

FIGURE 21

1 tcaatactat taattaataa ataaaaaaaa gcaaactaca aagaaaatgt caaggcgtaa
61 ctaaaaaaag ccataggctc ctataggcaa tgaaacaaat cttgattttg tattacaaaa
121 tctagaagtt tacaaaagcc agattgagca ttataagacc tagtagtaat agatcaaaga
181 ggaggatctc aagcttttaa agttcaaaaa ttaagattag gatggaaact ctggcaacga
241 tgatgatgat gaagaaaaca actcaaataa ataataagaa ttattaagga gagtcaatta
301 gattaagtag caagtttaat tgataaaaaa agttggttct aaggtagaga aagatttgaa
361 tttgaacgaa gatgaaaaca aaaagaatgg actttctgaa tagcaagtga aagaagagta
421 attaagaacg attactgaag aataggttaa gtattaaaat ttagtattta acatggacta
481 ccagttagat ttaaatgaga gtggtggcca tagaagacac agaagagaaa cagattatga
541 tactgaaaaa tggtttgaaa tatctcatga ccaaaaaaat tatgtatcaa tttacgccaa
601 ctaaaagaca tcatattgtt ggtggcttaa agattatttt aataaaaaca attatgatca
661 tcttaatgta agcattaaca gactagaaac tgaagccgaa ttctatgcct ttgatgattt
721 ttcacaaaca atcaaactta ctaataattc ttactagact gttaacatag acgttaattt
781 tgataataat ctctgtatac tcgcattgct tagattttta ttatcactag aaagattcaa
841 tattttgaat ataagatctt cttatacaag aaattaatat aattttgaga aaattggtga
901 gctacttgaa actatcttcg cagttgtctt ttctcatcgc cacttacaag gcattcattt
961 acaagttcct tgcgaagcgt tctaatattt agttaactcc tcatcataaa ttagcgttaa
1021 agatagctaa ttataggtat actctttctc tacagactta aaattagttg acactaacaa
1081 agtccaagat tattttaagt tcttataaga attccctcgt ttgactcatg taagctagta
1141 ggctatccca gttagtgcta ctaacgctgt agagaacctc aatgttttac ttaaaaaggt
1201 caagcatgct aatcttaatt tagtttctat ccctacctaa ttcaattttg atttctactt
1261 tgttaattta taacatttga aattagagtt tggattagaa ccaaatattt tgacaaaaca
1321 aaagcttgaa aatctacttt tgagtataaa ataatcaaaa aatcttaaat ttttaagatt
1381 aaacttttac acctacgttg cttaagaaac ctccagaaaa cagatattaa aacaagctac
1441 aacaatcaaa aatctcaaaa acaataaaaa tcaagaagaa actcctgaaa ctaaagatga
1501 aactccaagc gaaagcacaa gtggtatgaa attttttgat catctttctg aattaaccga
1561 gcttgaagat ttcagcgtta acttgtaagc tacccaagaa atttatgata gcttgcacaa
1621 acttttgatt agatcaacaa atttaaagaa gttcaaatta agttacaaat atgaaatgga
1681 aaagagtaaa atggatacat tcatagatct taagaatatt tatgaaacct taaacaatct
1741 taaaagatgc tctgttaata tatcaaatcc tcatggaaac atttcttatg aactgacaaa
1801 taaagattct actttttata aatttaagct gaccttaaac taagaattat aacacgctaa
1861 gtatactttt aagtagaacg aattttaatt taataacgtt aaaagtgcaa aaattgaatc
1921 ttcctcatta gaaagcttag aagatattga tagtctttgc aaatctattg cttcttgtaa
1981 aaatttacaa aatgttaata ttatcgccag tttgctctat cccaacaata tttagaaaaa
2041 tcctttcaat aagcccaatc ttctattttt caagcaattt gaataattga aaaatttgga
2101 aaatgtatct atcaactgta ttcttgatca gcatatactt aattctattt cagaattctt
2161 agaaaagaat aaaaaaataa aagcattcat tttgaaaaga tattatttat tacaatatta
2221 tcttgattat actaaattat ttaaaacact tcaatagtta cctgaattaa attaagttta
2281 cattaattag caattagaag aattgactgt gagtgaagta cataagtaag tatgggaaaa
2341 ccacaagcaa aaagctttct atgaaccatt atgtgagttt atcaaagaat catcctaaac
2401 cctttagcta atagattttg accaaaacac tgtaagtgat gactctatta aaaagatttt
2461 agaatctata tctgagtcta agtatcatca ttatttgaga ttgaacccta gttaatctag
2521 cagtttaatt aaatctgaaa acgaagaaat ttaagaactt ctcaaagctt gcgacgaaaa
2581 aggtgtttta gtaaaagcat actataaatt ccctctatgt ttaccaactg gtacttatta
2641 cgattacaat tcagatagat ggtgattaat taaatattag tttaaataaa tattaaatat
2701 tgaatatttc tttgcttatt atttgaataa tacatacaat agtcattttt agtgttttga
2761 atatatttta gttatttaat tcattatttt aagtaaataa ttatttttca atcatttttt
2821 aaaaaatcg

FIGURE 22

MSRRNQKKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQQIK

EEDLKLLKFKNQDQDGNSGNDDDEENNSNKQQELLRRVNQIKQQVQLIKKVGSKVEK

DLNLNEDENKKNGLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRR

ETDYDTEKWFEISHDQKNYVSIYANQKTSYCWWLKDYFNKNNYDHLNVSINRLETEAE

FYAFDDFSQTIKLTNNSYQTVNIDVNFDNNLCILALLRFLLSLERFNILNIRSSYTRN

QYNFEKIGELLETIFAVVFSHRHLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQVYSF

STDLKLVDTNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENLNVLLKKVKHANLNL

VSIPTQFNFDFYFVNLQHLKLEFGLEPNILTKQKLENLLLSIKQSKNLKFLRLNFYTY

VAQETSRKQILKQATTIKNLKNNKNQEETPETKDETPSESTSGMKFFDHLSELTELED

FSVNLQATQEIYDSLHKLLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNIYETLNNLK

RCSVNISNPHGNISYELTNKDSTFYKFKLTLNQELQHAKYTFKQNEFQFNNVKSAKIE

SSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNPFNKPNLLFFKQFEQLK

NLENVSINCILDQHILNSISEFLEKNKKIKAFILKRYYLLQYYLDYTKLFKTLQQLPE

LNQVYINQQLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDFDQNTVSD

DSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQELLKACDEKGVLVKAYYKFP

LCLPTGTYYDYNSDRW

FIGURE 23

MKILFEFIQDKLDIDLQTNSTYKENLKCGHFNGLDEILTTCFAL

PNSRKIALPCLPGDLSHKAVIDHCIIYLLTGELYNNVLTFGYKIARNEDVNNSLFCHS

ANVNVTLLKGAAWKMFHSLVGTYAFVDLLINYTVIQFNGQFFTQIVGNRCNEPHLPPK

WVQRSSSSSATAAQIKQLTEPVTNKQFLHKLNINSSSFFPYSKILPSSSSIKKLTDLR

EAIFPTNLVKIPQRLKVRINLTLQKLLKRHKRLNYVSILNSICPPLEGTVLDLSHLSR

QSPKERVLKFIIVILQKLLPQEMFGSKKNKGKIIKNLNLLLSLPLNGYLPFDSLLKKL

RLKDFRWLFISDIWFTKHNFENLNQLAICFISWLFRQLIPKIIQTFFYCTEISSTVTI

VYFRHDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLSNFNHSKMRIIPKKSNNEFR

IIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKE

FKQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFN

TNTGVLKLFNVVNASRVPKPYELYIDNVRTVHLSNQDVINVVEMEIFKTALWVEDKCY

IREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPSQDTLILKLADDFLIISTDQQQV

INIKKLAMGGFQKYNAKANRDKILAVSSQSDDDTVIQFCAMHIFVKELEVWKHSSTMN

NFHIRSKSSKGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISECYKSAF

KDLSINVTQNMQFHSFLQRIIEMTVSGCPITKCDPLIEYEVRFTILNGFLESLSSNTS

KFKDNIILLRKEIQHLQAYIYIYIHIVN

FIGURE 24

Oxytricha	LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
Euplotes	LCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLT

FIGURE 25

```
                                                     Motif 0
human                              AKFLHWLMSVYVVELLRSFFYVTETTFQKNR
tez1       ISEIEWLVLGKRSNAKMCLSDFEKRKQIFAEFIYWLYNSFIIPILQSFFYITESSDLRNR
EST2       LKDFRWLFISD---IWFTKHNFENLNQLAICFISWLFRQLIPKIIQTFFYCTEISSTVT-
p123       TREISWMQVET-SAKHFYYFDHEN-IYVLWKLLRWIFEDLVVSLIRCFFYVTEQQKSYSK
                                           . *.    .  ....*** **

                                                         Motif 1
human      LFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPALLTSRLRFIPKP--DGL
tez1       TVYFRKDIWKLLCRPFI-TSMKHEAFEKINENNVRMDTQK-TTLPPAVIRLLPKK--NTF
EST2       IVYFRHDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLS--NFNHSKMRIIPKKSNNEF
p123       TYYYRKNIWDVIMKHSI-ADLKKETLAEVQEKEVEEWKKS-LGFAPGKLRLIPKK--TTF
             ..*.  *  .    *    *                          .*  .**

           Motif 2
human      RPIVNMDYVVGARTFRREKRAERLTSRVKALP-SVLNYERA
tez1       RLITN-LRKRFLIKMGSNKKMLVSTNQTLRPVASILKHLINEESSGIPFNLEVYMKLLTF
EST2       RIIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKEF
p123       RPIMTFNKKIVNSDRKTTKLTTNTKLLNSHLMLKTLKN-RMFKDPPGFAVFNYDDVMKKY
           * *               *                *      .             .  .

                             Motif 3 (A)
tez1       KKDLLKHRMFGR-KKYFVRIDIKSCYDRIKQDLMFRIVKK-KLKDPEFVIRKYATIHATS
EST2       KQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKD-ALKNENGFFVRSQYFFNTN
p123       EEFVCKWKQVGQPKLFFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKN
              . *         .*   *   *** . .      .*   *
```

FIGURE 26

ATTTATACTCATGAAAATCTTATTCGAGTTCATTCAAGACAAGCTTGACATTGATCTACA
GACCAACAGTACTTACAAAGAAAATTTAAAATGTGGTCACTTCAATGGCCTCGATGAAAT
TCTAACTACGTGTTTCGCACTACCAAATTCAAGAAAAATAGCATTACCATGCCTTCCTGG
TGACTTAAGCCACAAAGCAGTCATTGATCACTGCATCATTTACCTGTTGACGGGCGAATT
ATACAACAACGTACTAACATTTGGCTATAAAATAGCTAGAAATGAAGATGTCAACAATAG
TCTTTTTTGCCATTCTGCAAATGTTAACGTTACGTTACTGAAAGGCGCTGCTTGGAAAAT
GTTCCACAGTTTGGTCGGTACATACGCATTCGTTGATTTATTGATCAATTATACAGTAAT
TCAATTTAATGGGCAGTTTTTCACTCAAATCGTGGGTAACAGATGTAACGAACCTCATCT
GCCGCCCAAATGGGTCCAACGATCATCCTCATCATCCGCAACTGCTGCGCAAATCAAACA
ACTTACAGAACCAGTGACAAATAAACAATTCTTACACAAGCTCAATATAAATTCCTCTTC
TTTTTTTCCTTATAGCAAGATCCTTCCTTCATCATCATCTATCAAAAAGCTAACTGACTT
GAGAGAAGCTATTTTTCCCACAAATTTGGTTAAAATTCCTCAGAGACTAAAGGTACGAAT
TAATTTGACGCTGCAAAAGCTATTAAAGAGACATAAGCGTTTGAATTACGTTTCTATTTT
GAATAGTATTTGCCCACCATTGGAAGGGACCGTATTGGACTTGTCGCATTTGAGTAGGCA
ATCACCAAAGGAACGAGTCTTGAAATTTATCATTGTTATTTTACAGAAGTTATTACCCCA
AGAAATGTTTGGCTCAAAGAAAAATAAAGGAAAAATTATCAAGAATCTAAATCTTTTATT
AAGTTTACCCTTAAATGGCTATTTACCATTTGATAGTTTGTTGAAAAAGTTAAGATTAAA
GGATTTTCGGTGGTTGTTCATTTCTGATATTTGGTTCACCAAGCACAATTTTGAAAACTT
GAATCAATTGGCGATTTGTTTCATTTCCTGGCTATTTAGACAACTAATTCCCAAAATTAT
ACAGACTTTTTTTTACTGCACCGAAATATCTTCTACAGTGACAATTGTTTACTTTAGACA
TGATACTTGGAATAAACTTATCACCCCTTTTATCGTAGAATATTTTAAGACGTACTTAGT
CGAAAACAACGTATGTAGAAACCATAATAGTTACACGTTGTCCAATTTCAATCATAGCAA
AATGAGGATTATACCAAAAAAAAGTAATAATGAGTTCAGGATTATTGCCATCCCATGCAG
AGGGGCAGACGAAGAAGAATTCACAATTTATAAGGAGAATCACAAAAAATGCTATCCAGCC
CACTCAAAAAATTTTAGAATACCTAAGAAACAAAAGGCCGACTAGTTTTACTAAAATATA
TTCTCCAACGCAAATAGCTGACCGTATCAAAGAATTTAAGCAGAGACTTTTAAAGAAATT
TAATAATGTCTTACCAGAGCTTTATTTCATGAAATTTGATGTCAAATCTTGCTATGATTC
CATACCAAGGATGGAATGTATGAGGATACTCAAGGATGCGCTAAAAAATGAAAATGGGTT
TTTCGTTAGATCTCAATATTTCTTCAATACCAATACAGGTGTATTGAAGTTATTTAATGT
TGTTAACGCTAGCAGAGTACCAAAACCTTATGAGCTATACATAGATAATGTGAGGACGGT
TCATTTATCAAATCAGGATGTTATAAACGTTGTAGAGATGGAAATATTTAAAACAGCTTT
GTGGGTTGAAGATAAGTGCTACATTAGAGAAGATGGTCTTTTTCAGGGCTCTAGTTTATC
TGCTCCGATCGTTGATTTGGTGTATGACGATCTTCTGGAGTTTTATAGCGAGTTTAAAGC
CAGTCCTAGCCAGGACACATTAATTTTAAAACTGGCTGACGATTTCCTTATAATATCAAC
AGACCAACAGCAAGTGATCAATATCAAAAAGCTTGCCATGGGCGGATTTCAAAAATATAA
TGCGAAAGCCAATAGAGACAAAATTTTAGCCGTAAGCTCCCAATCAGATGATGATACGGT
TATTCAATTTTGTGCAATGCACATATTTGTTAAAGAATTGGAAGTTTGGAAACATTCAAG
CACAATGAATAATTTCCATATCCGTTCGAAATCTAGTAAAGGGATATTTCGAAGTTTAAT
AGCGCTGTTTAACACTAGAATCTCTTATAAAACAATTGACACAAATTTAAATTCAACAAA
CACCGTTCTCATGCAAATTGATCATGTTGTAAAGAACATTTCGGAATGTTATAAATCTGC
TTTTAAGGATCTATCAATTAATGTTACGCAAAATATGCAATTTCATTCGTTCTTACAACG
CATCATTGAAATGACAGTCAGCGGTTGTCCAATTACGAAATGTGATCCTTTAATCGAGTA
TGAGGTACGATTCACCATATTGAATGGATTTTTGGAAAGCCTATCTTCAAACACATCAAA
ATTTAAAGATAATATCATTCTTTTGAGAAAGGAAATTCAACACTTGCAAGC

FIGURE 27

AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKR
VQLRDVSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKR
AERLTSRVKALFSVLNYERA

FIGURE 28

GCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTC
TTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACC
GGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAA
GAGGGTGCAGCTGCGGGACGTGTCGGAAGCAGAGGTCAGGCAGCATCGGGA
AGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGACG
GGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCG
CAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGC
GTGCTCAACTACGAGCGGGCGCG

FIGURE 29

MTEHHTPKSRILRFLENQYVYLCTLNDYVQLVLRGSPASSYSNICERLRSDVQTSFSIFLHSTVVGF
DSKPDEGVQFSSPKCSQSELIANVVKQMFDESFERRRNLLMKGFSMNHEDFRAMHVNGVQNDLV
STFPNYLISILESKNWQLLLEIIGSDAMHYLLSKGSIFEALPNDNYLQISGIPLFKNNVFEETVSKKRK
RTIETSITQNKSARKEVSWNSISISRFSIFYRSSYKKFKQDLYFNLHSICDRNTVHMWLQWIFPRQFG
LINAFQVKQLHKVIPLVSQSTVVPKRLLKVYPLIEQTAKRLHRISLSKVYNHYCPYIDTHDDEKILS
YSLKPNQVFAFLRSILVRVFPKLIWGNQRIFEIILKDLETFLKLSRYESFSLHYLMSNIKISEIEWLVL
GKRSNAKMCLSDFEKRKQIFAEFIYWLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIWKLLCRPFIT
SMKMEAFEKINENNVRMDTQKTTLPPAVIRLLPKKNTFRLITNLRKRFLIKMGSNKKMLVSTNQT
LRPVASILKHLINEESSGIPFNLEVYMKLLTFKKDLLKHRMFGRKKYFVRIDIKSCYDRIKQDLMFR
IVKKKLKDPEFVIRKYATIHATSDRATKNFVSEAFSYFDMVPFEKVVQLLSMKTSDTLFVDFVDY
WTKSSSEIFKMLKEHLSGHIVKIGNSQYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTKKKGSVL
LRVVDDFLFITVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENSNGIINNTFFNESKKRMPFFG
FSVNMRSLDTLLACPKIDEALFNSTSVELTKHMGKSFFYKILRSSLASFAQVFIDITHNSKFNSCCNI
YRLGYSMCMRAQAYLKRMKDIFIPQRMFITDLLNVIGRKIWKKLAEILGYTSRRFLSSAEVKWLFC
LGMRDGLKPSFKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLFLHRRIAD

FIGURE 30

ggtaccgattacttccttcttcataagctaattgcttcctcgaacgctcctaaatctctggaaatatttttacaagaactcaataacaataccaagtcaaattccaatatgaagg
tgttattagtgatcgataatattctatttatcggtcgttaccaagtataaggacaaaaagaacaacttccttcccccctaaagactttacttattaattactttcaaatatattcg
ggttcgcttactttaatcgtggtactgtttagctgctacttctagccaaccgcgtgttctaccccgtcattggatatagctcttggagtagctcacagaaatccttacaaatctt
ctgatgagactatattagattcattacagtccgtgcatattcttaacatggagccttacactttagatgagtcacgtcgcatgatggagtattggtatcatccaacgtttgccttg
aaaaggttgataattatttgcaaaatcatgtccttagtggtggtaatccgcgaaagtttttttgatgcttgcacacgtctagcatgattgagatattcaaaaatttctatccactacaa
ctccttaacgcggtttatttttctatttctattctcatgttgttccaaatatgtatcatctcgtattaggcttttttccgtttactcctggaatcgtaccttttcactattccccctaatg
aataatctaaattagtttcgcttataattgatagtagtagaaagattggtgattctactcgtgtaatgttattagttaaagatactttgcaaaacattattagctatcattatataaaa
aaaatcctataattataaatattaatcaatatttgcggtcactatttatttaaaacgttatgatcagtaggacactttgcatatatatagttatgcttaatggttacttgtaacttgcAT
GACCGAACACCATACCCCCAAAAGCAGGATTCTTCGCTTTCTAGAGAATCAATATGTATACCTATGTA
CCTTAAATGATTATGTACAACTTGTTTTGAGAGGGTCGCCGGCAAGCTCGTATAGCAATATATGCGAA
CGCTTGAGAAGCGATGTACAAACGTCCTTTTCTATTTTTCTTCATTCGACTGTAGTCGGCTTCGACAGT
AAGCCAGATGAAGGTGTTCAATTTTCTTCTCCAAAATGCTCACAGTCAGAGgtatatatatttgtttgatttttttctattcg
ggatagctaatatatgggcagCTAATAGCGAATGTTGTAAAACAGATGTTCGATGAAAGTTTTGAGCGTCGAAGGA
ATCTACTGATGAAAGGGTTTTCCATGgtaaggtattctaattgtgaaatattacctgcaattactgtttcaaagagattgtattaaccgataaagAA
TCATGAAGATTTTCGAGCCATGCATGTAAACGGAGTACAAAATGATCTCGTTTCTACTTTTCCTAATTA
CCTTATATCTATACTTGAGTCAAAAAATTGGCAACTTTTGTTAGAAATgtaaataccggttaagatgttgcgcactttgaaca
agactgacaagtatagTATCGGCAGTGATGCCATGCATTACTTATTATCCAAAGGAAGTATTTTTGAGGCTCTTC
CAAATGACAATTACCTTCAGATTTCTGGCATACCACTTTTTAAAAATAATGTGTTTGAGGAAACTGTGT
CAAAAAAAAGAAAGCGAACCATTGAAACATCCATTACTCAAAATAAAAGCGCCCGCAAAGAAGTTTC
CTGGAATAGCATTTCAATTAGTAGGTTTAGCATTTTTTACAGGTCATCCTATAAGAAGTTTAAGCAAGgt
aactaatactgttatccttcataactaatttagATCTATATTTTAACTTACACTCTATTTGTGATCGGAACACAGTACACATG
TGGCTTCAATGGATTTTTCCAAGGCAATTTGGACTTATAAACGCATTTCAAGTGAAGCAATTGCACAA
AGTGATTCCACTGGTATCACAGAGTACAGTTGTGCCCAAACGTCTCCTAAAGGTATACCCTTTAATTGA
ACAAACAGCAAAGCGACTCCATCGTATTTCTCTATCAAAAGTTTACAACCATTATTGCCCATATATTGA
CACCCACGATGATGAAAAAATCCTTAGTTATTCCTTAAAGCCGAACCAGGTGTTTGCGTTTCTTCGATC
CATTCTTGTTCGAGTGTTTCCTAAATTAATCTGGGGTAACCAAAGGATATTTGAGATAATATTAAAAGg
tattgtataaaattattaccactaacgatttaccagACCTCGAAACTTTCTTGAAATTATCGAGATACGAGTCTTTTAGTTTAC
ATTATTTAATGAGTAACATAAAGgtaatatgccaaattttttaccattaattaacaatcagATTTCAGAAATTGAATGGCTAGT
CCTTGGAAAAAGGTCAAATGCGAAAATGTGCTTAAGTGATTTTGAGAAACGCAAGCAAATATTTGCGG
AATTCATCTACTGGCTATACAATTCGTTTATAATACCTATTTTACAATCTTTTTTTTATATCACTGAATC
AAGTGATTTACGAAATCGAACTGTTTATTTTAGAAAAGATATTTGGAAACTCTTGTGCCGACCCTTTAT
TACATCAATGAAAATGGAAGCGTTTGAAAAAATAAACGAGgtatttaaagtatttttgcaaaaagctaatatttcagAACAA
TGTTAGGATGGATACTCAGAAAACTACTTTGCCTCCAGCAGTTATTCGTCTATTACCTAAGAAGAATAC
CTTTCGTCTCATTACGAATTTAAGAAAAAGATTCTTAATAAAGgtattaatttttggtcatcaatgtacttacttctaatctattattag
cagATGGGTTCAAACAAAAAAATGTTAGTCAGTACGAACCAAACTTTACGACCTGTGGCATCGATACTG
AAACATTTAATCAATGAAGAAAGTAGTGGTATTCCATTTAACTTGGAGGTTTACATGAAGCTTCTTACT
TTTAAGAAGGATCTTCTTAAGCACCGAATGTTTGGgtaattatataatgcgcgattcctcattattaatttgcagGCGTAAGAAG
TATTTTGTACGGATAGATATAAAATCCTGTTATGATCGAATAAAGCAAGATTTGATGTTTCGGATTGTT
AAAAAGAAACTCAAGGATCCCGAATTTGTAATTCGAAAGTATGCAACCATACATGCAACAAGTGACCG
AGCTACAAAAAACTTTGTTAGTGAGGCGTTTTCCTATTgtaagttatttttcattggaattttttaacaaattcttttagTTGATAT
GGTGCCTTTTGAAAAAGTCGTGCAGTTACTTTCTATGAAAACATCAGATACTTTGTTTGTTGATTTTGT
GGATTATTGGACCAAAAGTTCTTCTGAAATTTTTAAAATGCTCAAGGAACATCTCTCTGGACACATTGT
TAAGgtataccaattgttgaattgtaataacactaatgaaactagATAGGAAATTCTCAATACCTTCAAAAAGTTGGTATCCCTC
AGGGCTCAATTCTGTCATCTTTTTTTGTGTCATTTCTATATGGAAGATTTGATTGATGAATACCTATCGTT
TACGAAAAAGAAAGGATCAGTGTTGTTACGAGTAGTCGACGATTTCCTCTTTATAACAGTTAATAAAA
AGGATGCAAAAAAATTTTTGAATTTATCTTTAAGAGgtgagttgctgtcattcctaagttctaaccgttgaagGATTTGAGAA
ACACAATTTTTCTACGAGCCTGGAGAAAACAGTAATAAACTTTGAAAATAGTAATGGGATAATAAACA
ATACTTTTTTTAATGAAAGCAAGAAAAGAATGCCATTCTTCGGTTTCTCTGTGAACATGAGGTCTCTTG
ATACATTGTTAGCATGTCCTAAAATTGATGAAGCCTTATTTAACTCTACATCTGTAGAGCTGACGAAAC
ATATGGGGAAATCTTTTTTTTACAAAATTCTAAGgtatactgtgtaactgaataatagctgacaaataatcagATCGAGCCTTGC
ATCCTTTGCACAAGTATTTATTGACATTACCCACAATTCAAAATTCAATTCTTGCTGCAATATATATAG
GCTAGGATACTCTATGTGTATGAGAGCACAAGCATACTTAAAAAGGATGAAGGATATATTTATTCCCC
AAAGAATGTTCATAACGGgtgagtacttatttaactagaaaagtcattaattaaccttagATCTTTTGAATGTTATTGGAAGAAAA
ATTTGGAAAAAGTTGGCCGAAATATTAGGATATACGAGTAGGCGTTTCTTGTCCTCTGCAGAAGTCAA

FIGURE 31

```
EST2 pep              FFYCTEISST VTIVYFRHDT WN----KLIT P-----FIVE YFK-TYLVEN   40
Euplotes pep          FFYVTEQQKS YSKTYYYRKN IWDVI-MKMS IAD----LKK ETLA--EVQE   43
Trans of tetrahymen   ------KHKE GSQIFYYRKP IWKLVSKLTI VKVRIQFSEK NKQMKNNFYQ   44
Consensus             FFY.TE..K. .S..YYYRK. IW...-KL.. ...---F..K .......V..   50

EST2 pep              NVCRNHNSY- ---------- TLSNFNHSKM FLIIPKKSNNE FRIIAIPCRG   79
Euplotes pep          KEVEEWKKSL ---------- ---GFAPGKL RLIIPKKTT-- FRFIMTFNKK   78
Trans of tetrahymen   KIQLEEENLE KVEEKLIPED SFQKYPQGKL RLIIPKKGS-- FRFIMTFLRK   92
Consensus             K...E..... ---------- ....F..GKL RLIIPKK..-- FRFIMTF.RK  100

EST2 pep              ADEEEFTIYK ENHKNAIQPT QKILEYLRNK RPTSFTKIYS PTQIADRIKE  129
Euplotes pep          IVNSDRKTTK LTTNTKLLNS HLMLKTLKN- -------RMFK -DPFGFAVFN  120
Trans of tetrahymen   DKQKNIK--- LNLNQILMDS QLVFRNLKD- -------ML-G -QKIGYSVFD  130
Consensus             .......K..K LN.N..L..S QL.L..LKN- -------.... -..IG..VF.  150

EST2 pep              FKQRLLKKFN NVL------- -PELYFMKFD VKSCYD                  157
Euplotes pep          YD-DVMKKYE EFVCKWKQVG QPKLFFATMD IEKCYD                  155
Trans of tetrahymen   NK-QISEKFA QFIEKWKNKG RPQLYYVTL- ------                  158
Consensus             .K-...KKF. .F..KWK..G .P.LYF.T.D ...CYD                  186
```

FIGURE 32

S-1: FFY VTE TTF QKN RLF FYR KSV WSK
S-2: RQH LKR VQL RDV SEA EVR QHR EA
S-3: ART FRR EKR AER LTS RVK ALF SVL NYE

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q
A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS
A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV

FIGURE 33

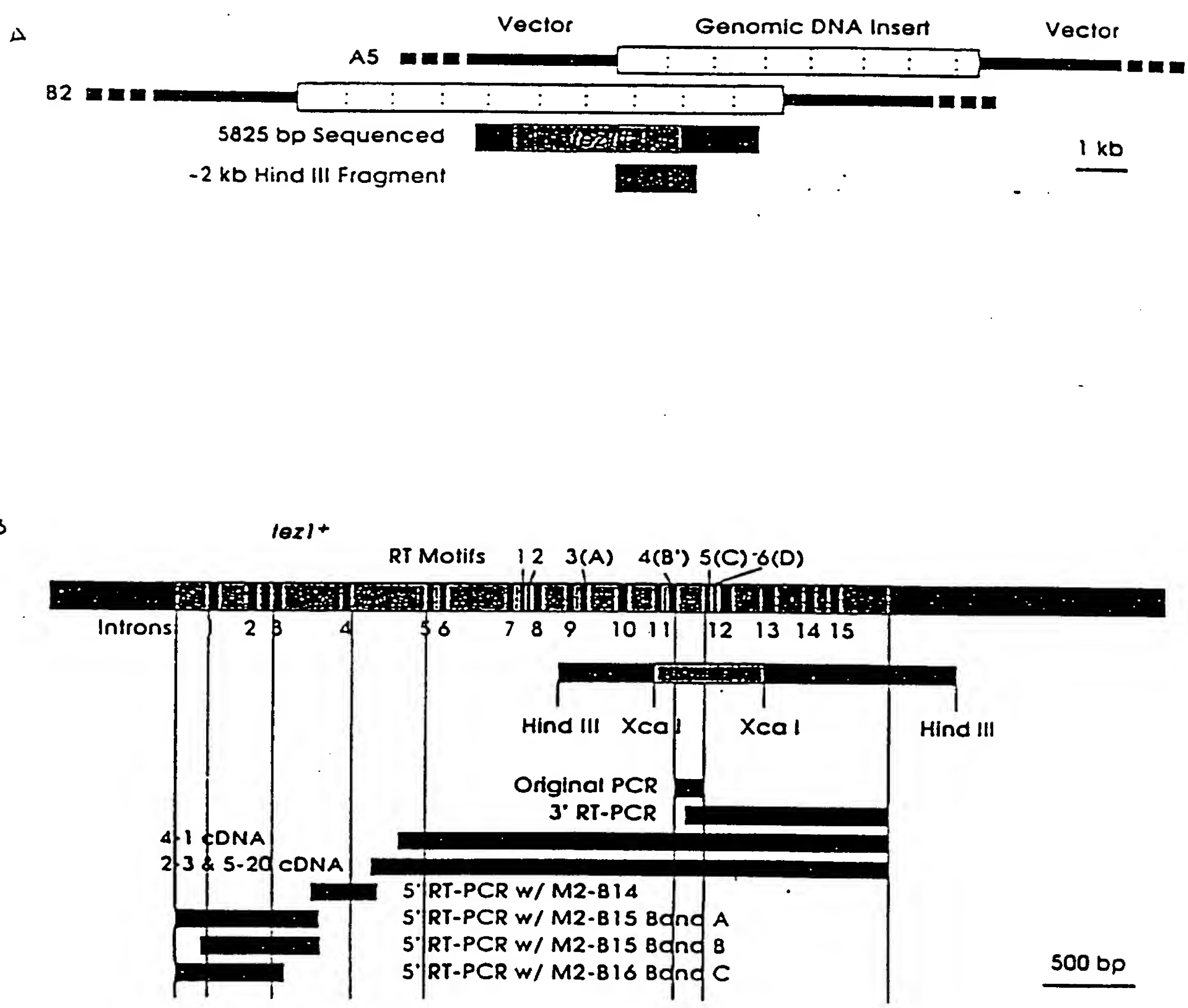

A
Vector
Genomic DNA Insert
Vector
A5
B2
5825 bp Sequenced
-2 kb Hind III Fragment
1 kb
B
lez1+
RT Motifs
1 2
3(A)
4(B')
5(C)
6(D)
Introns
2
3
4
5 6
7 8 9
10 11
12 13 14 15
Hind III
Xca I
Xca I
Hind III
Original PCR
3' RT-PCR
4-1 cDNA
2-3 & 5-20 cDNA
5' RT-PCR w/ M2-B14
5' RT-PCR w/ M2-B15 Band A
5' RT-PCR w/ M2-B15 Band B
5' RT-PCR w/ M2-B16 Band C
500 bp

FIGURE 34

<u>Poly 4</u>

```
              t         t         c
     t a      a    g    c    c    t c g
5'-  cag  acc aaa  gga  att  cca  taa gg  -3'
     Q    T   K    G    I    P    Q   G
```

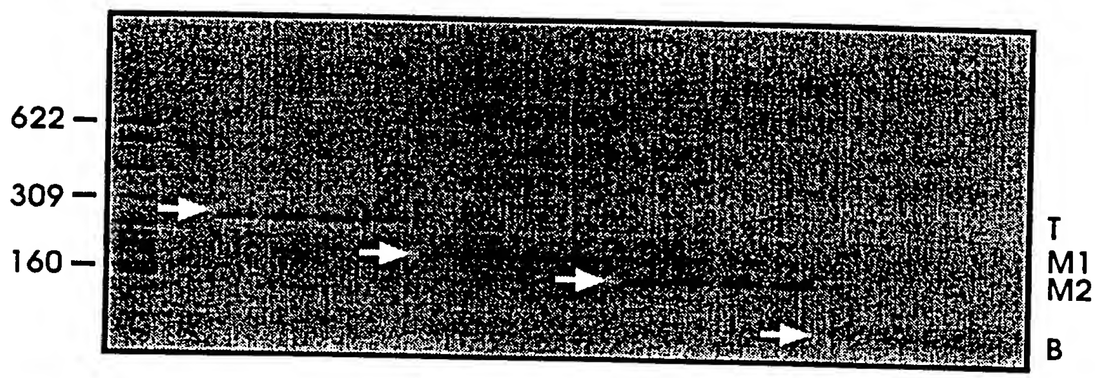
4 (B')

5 (C')

```
     D    D    Y    L    L    I    T
3'-  ctg  ctg  atg  gag  gag  tag  tgg  -5'
       a    a    a  a a  a a    a    a
                      t    t    t    t
                                c    c
```

<u>Poly 1</u>

FIGURE 35



Motif B' (4)

QTKGIPQG

Motif C (5)

DDYLLIT

FIGURE 36

PCR Product M2 showed Reasonable Match with Other Telomerase Proteins

```
Ot                LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
Ea_p123       KGIPQGLCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLIT
Sp_M2             SILSSFLCHFYMEDLIDEYLSFTKKK--------GSVLLRVV
Sc_p103       DGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS------QDTLILKLADDFLIIS
                   .*  .        *  .     *                   .....
```

```
 Q   K   V   G   I   P   Q   G
caa aaa gtt ggt atc cct cag gg......    <---Actual Genomic Sequence.
```

<u>Poly 4</u>

```
     t       t       c
t a   a   g   c   c   t c g
cag acc aaa gga att cca taa gg ---->

ag acc aaa gga att cca tca ggC TCA ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG
tc tgg ttt cct taa ggt agt ccG AGT TAA GAC AGT AGA AAA AAC ACA GTA AAG ATA TAC

        K   G   I   P   S   G   S   I   L   S   S   F   L   C   H   F   Y   M

GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA
CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC TTT CCT AGT CAC AAC AAT GCT

 E   D   L   I   D   E   Y   L   S   F   T   K   K   K   G   S   V   L   L   R

GTA GTC gac gac tac ctc ctc atc acc
CAT CAG ctg ctg atg gag gag tag tgg

 V   V   D   D   Y   L   L   I   T

  <---- ctg ctg atg gag gag tag tgg
          a   a   a a a a a   a   a
                    t   t   t   t
                    c   c
```

<u>Poly 1</u>

```
.....gac gat ttc ctc ttt ata aca......   <---Actual Genomic Sequence.
     D   D   F   L   F   I   T
```

FIGURE 37

3' RT PCR Strategy

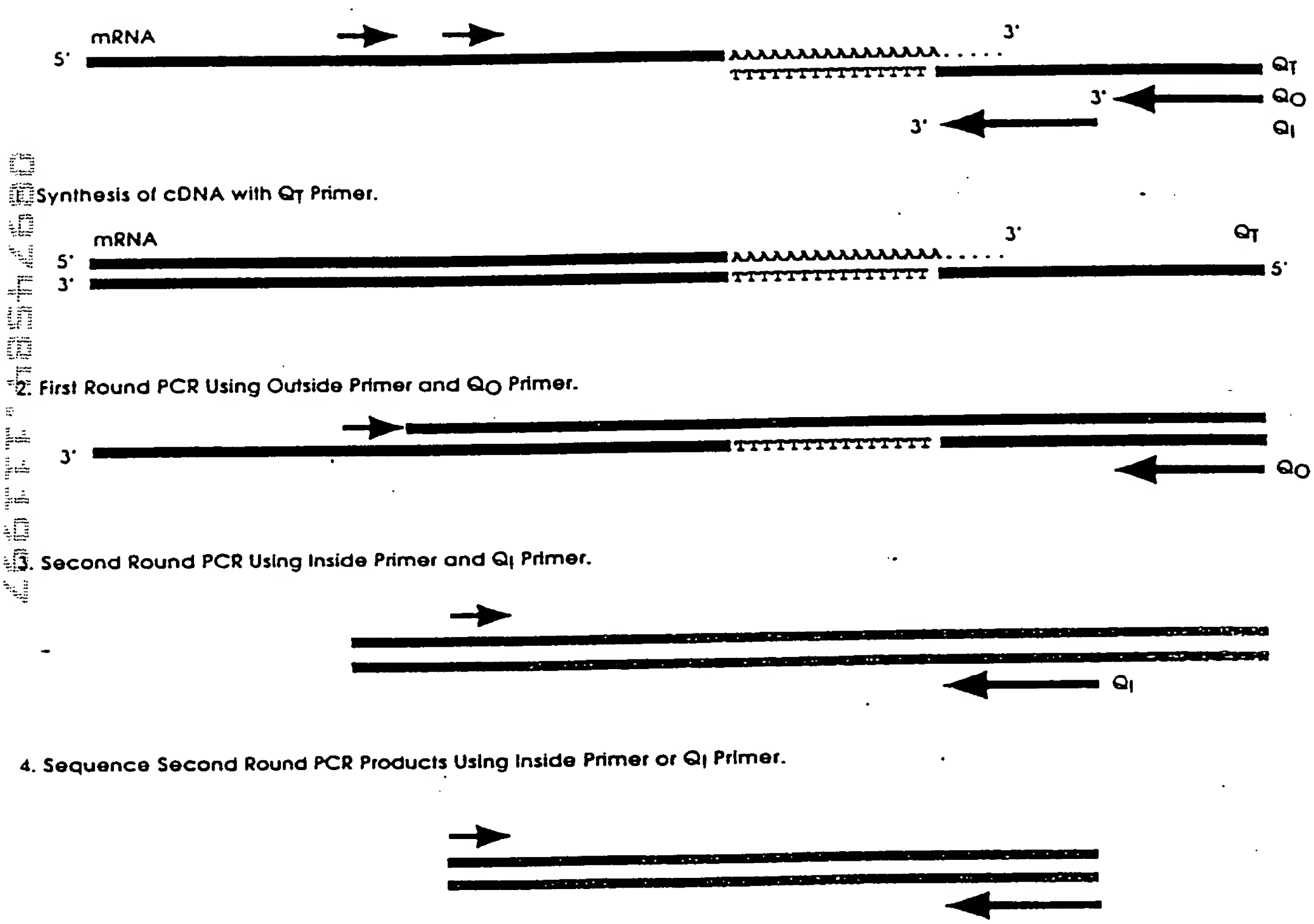


FIGURE 38

A

-Size Selected Libraries from P. Nurese

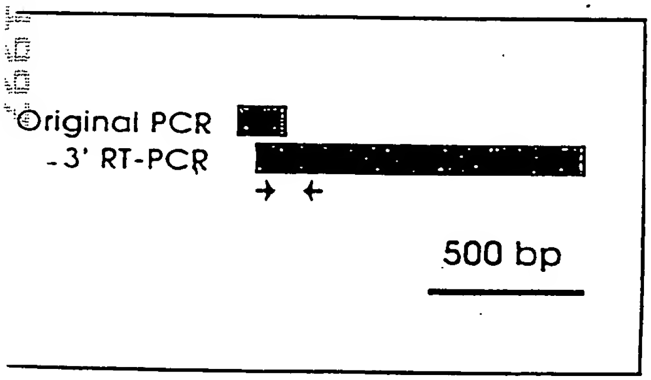
3 - 4 kb
5 - 6 kb
7 - 8 kb
11 - 12 kb

-Libraries from J.A. Wise

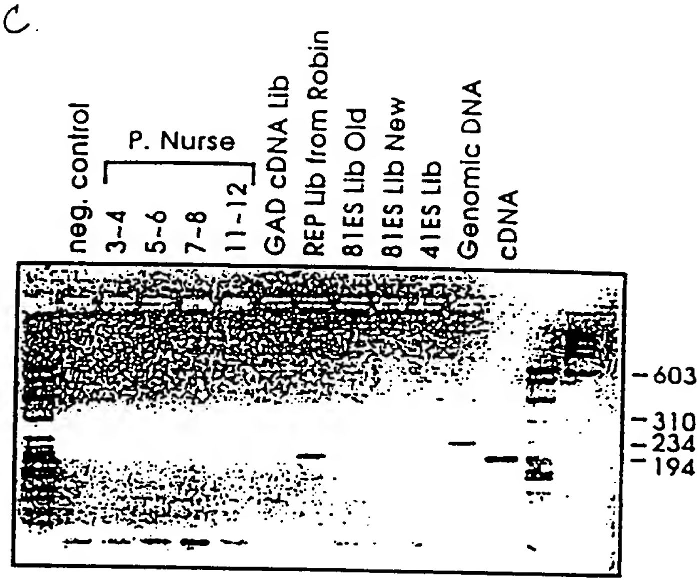
Sau 3a Partial Digest
Hind III Partial Digest

cDNA Libraries

GAD (Gal Activation Domain) Library
REP Library from R. Allshire
REP81ES Library (old)
REP81ES Library (new)
REP41ES Library



C.



D.

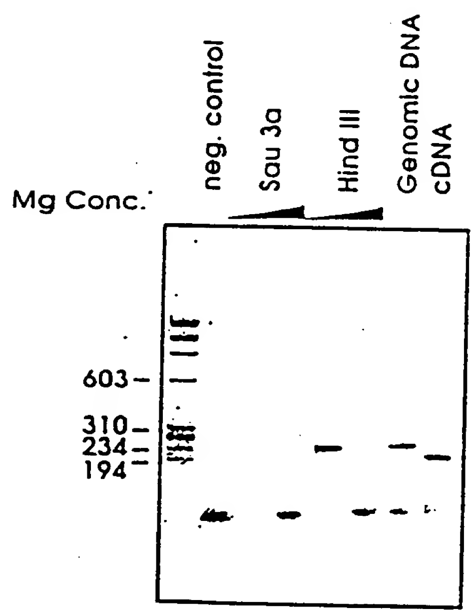
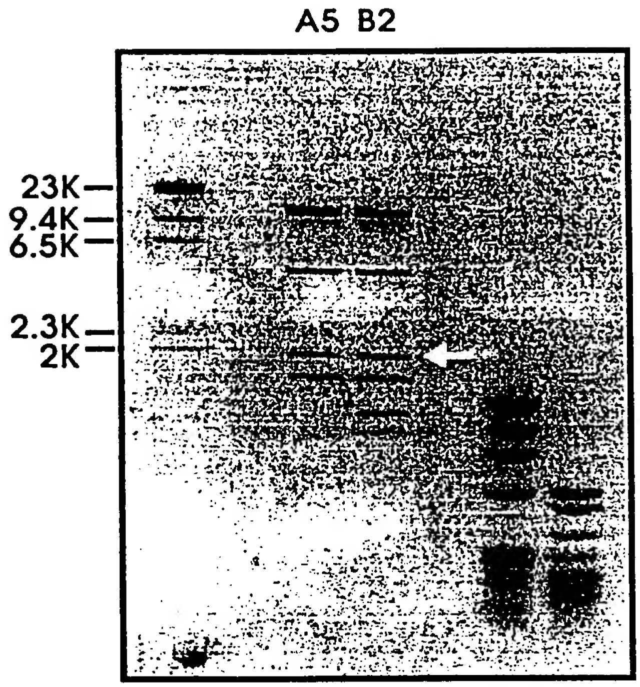


FIGURE 39



Hind III Digested Positive Genomic Clones

FIGURE 40

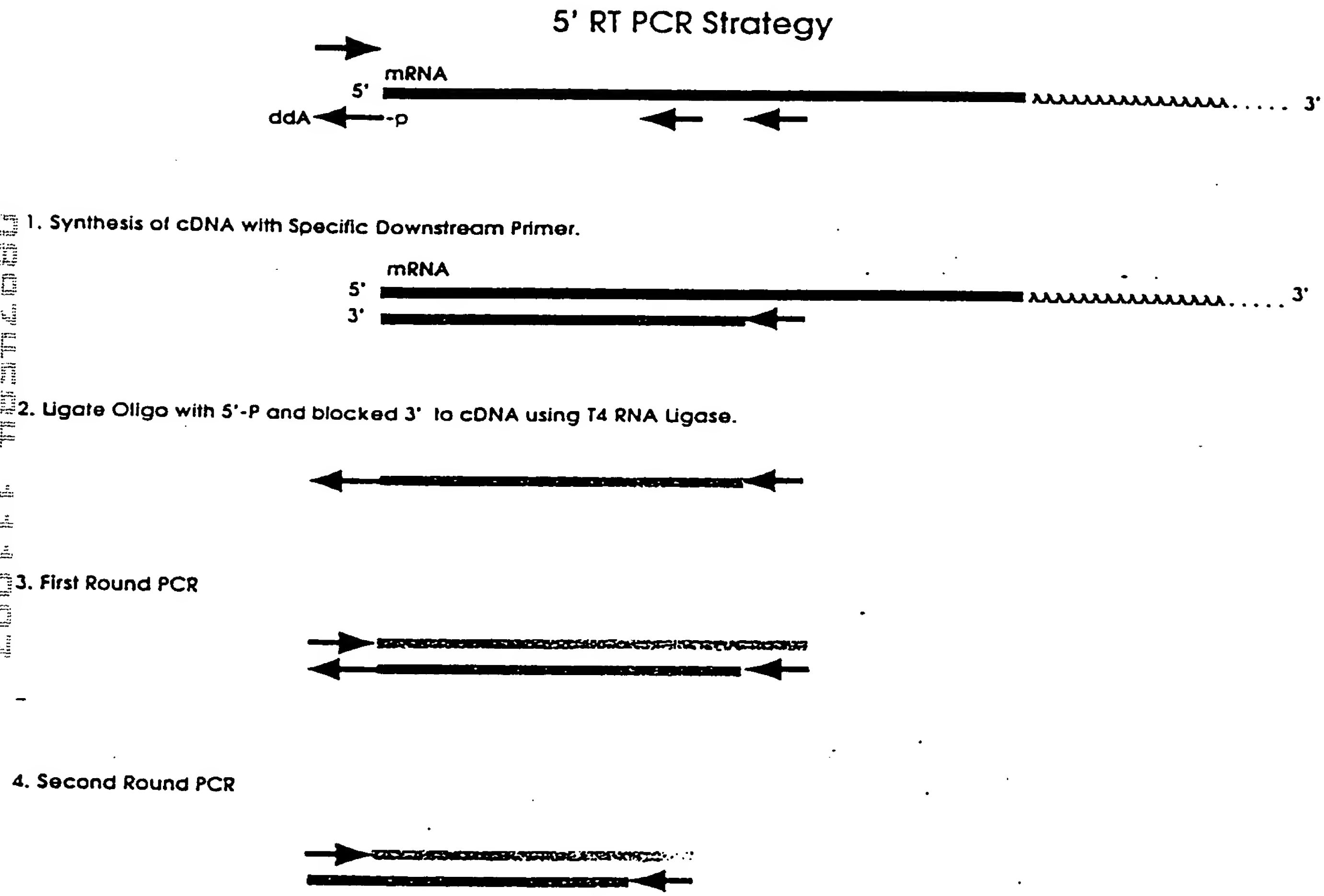

5' RT PCR Strategy
mRNA
5'
3'
ddA
-p
1. Synthesis of cDNA with Specific Downstream Primer.
mRNA
5'
3'
3'
2. Ligate Oligo with 5'-P and blocked 3' to cDNA using T4 RNA Ligase.
3. First Round PCR
4. Second Round PCR

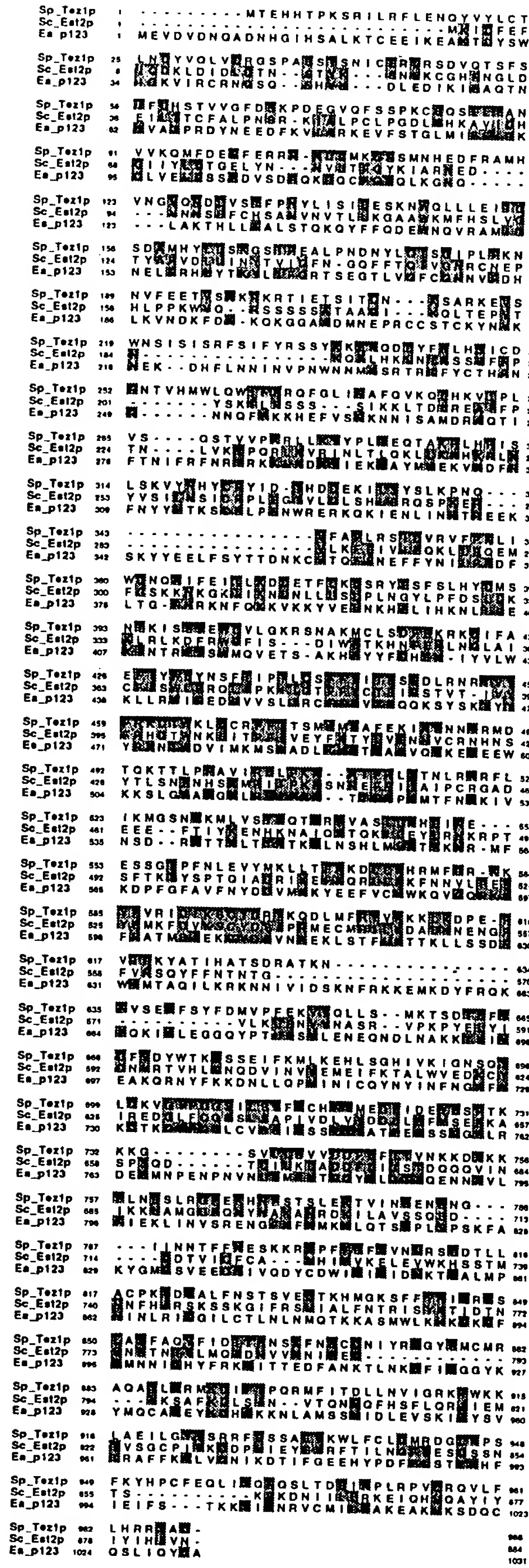
FIGURE 41

Alignment of RT Domains from Telomerase Catalytic Subunits.

```
                                 Motif O
S.p. Tez1p (429). WLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIW ...(35)...
S.c. Est2p (366). WLFRQLIPKIIQTFFYCTEISSTVT-IVYFRHDTW ...(35)...
E.a. p123  (441). WIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIW ...(35)...
                  *                ***  **           *  *    *

                Motif 1     Motif 2      K
                p hh h K     hR h        R
S.p. Tez1p      AVIRLLPKK--NTFRLITN-LRKRF ...(61)...
S.c. Est2p      SKMRIIPKKSNNEFRIIAIPCRGAD ...(62)...
E.a. p123       GKLRLIPKK--TTFRPIMTFNKKIV ...(61)...
                  *  ***     ** *

                Motif 3(A) AF
                   h  hDh  GY  h
S.p. Tez1p      KKYFVRIDIKSCYDRIKQDLMFRIVK ...(89)...
S.c. Est2p      ELYFMKFDVKSCYDSIPRMECMRILK ...(75)...
E.a. p123       KLFFATMDIEKCYDSVNREKLSTFLK ...(107)...
                   *   *   ***           *

                 Motif 4(B')
                      hPQG    pP hh    h
S.p. Tez1p      YLQKVGIPQGSILSSFLCHFYMEDLIDEYLSF ...(6)...
S.c. Est2p      YIREDGLFQGSSLSAPIVDLVYDDLLEFYSEF ...(8)...
E.a. p123       YKQTKGIPQGLCVSSILSSFYYATLEESSLGF ...(14)...
                *    * **    *          *      *

                   Y Motif 5(C)                        Motif 6(D)
                h   F DDhhh                            Gh h  cK   h
S.p. Tez1p      VLLRVVDDFLFITVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENS .(205)
S.c. Est2p      LILKLADDFLIISTDQQQVINIKKLAMGGFQKYNAKANRDKILAVSSQS .(173)
E.a. p123       LLMRLTDDYLLITTQENNAVLFIEKLINVSRENGFKFNMKKLQTSFPLS .(209)
                     ** *  *                              *      *
```

Figure 42

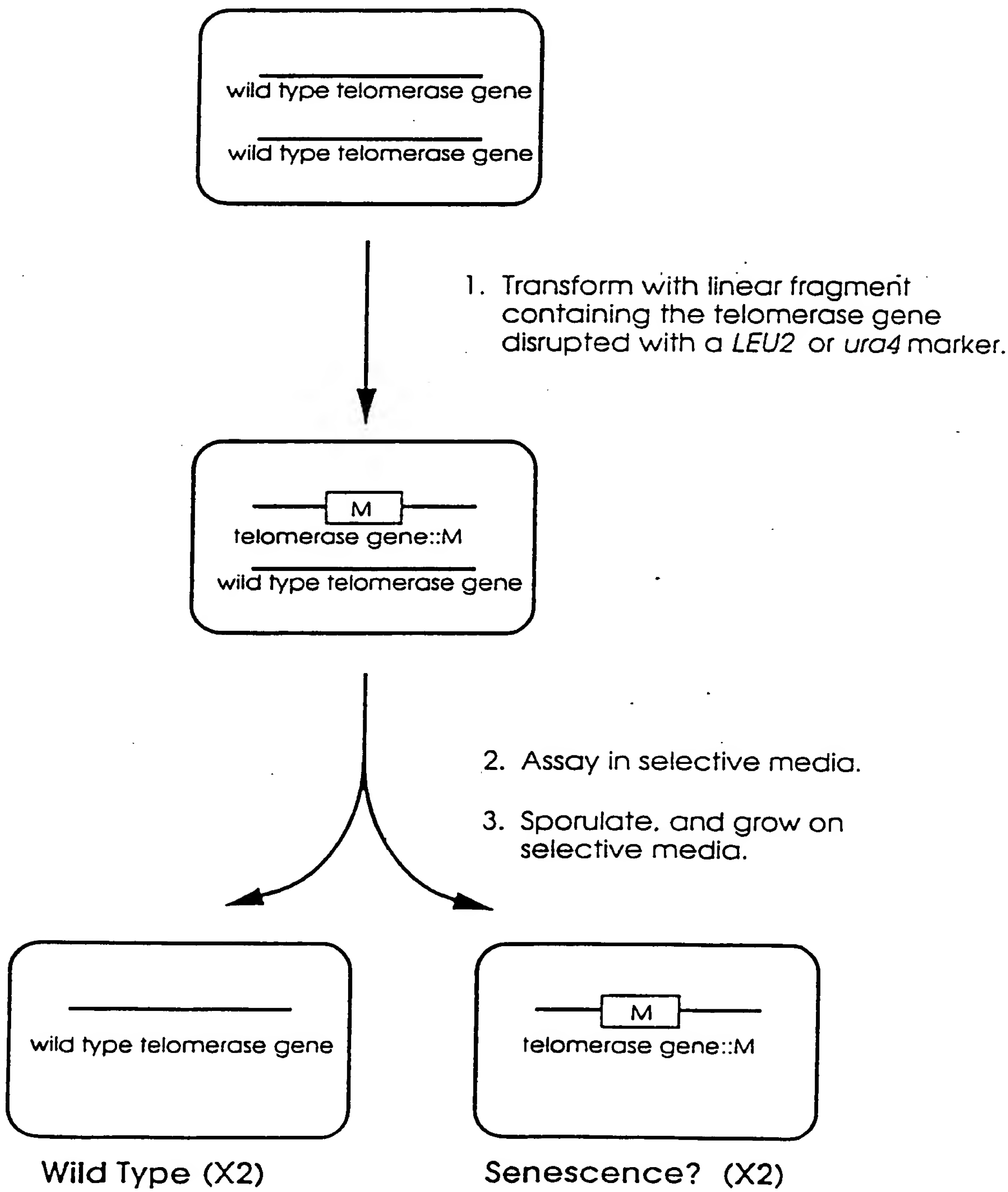
A



1/2

FIGURE 43

Disruption strategy for the putative telomerase genes.



(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)

Figure 44

An Example of Confirmation of tez1 disruption By PCR

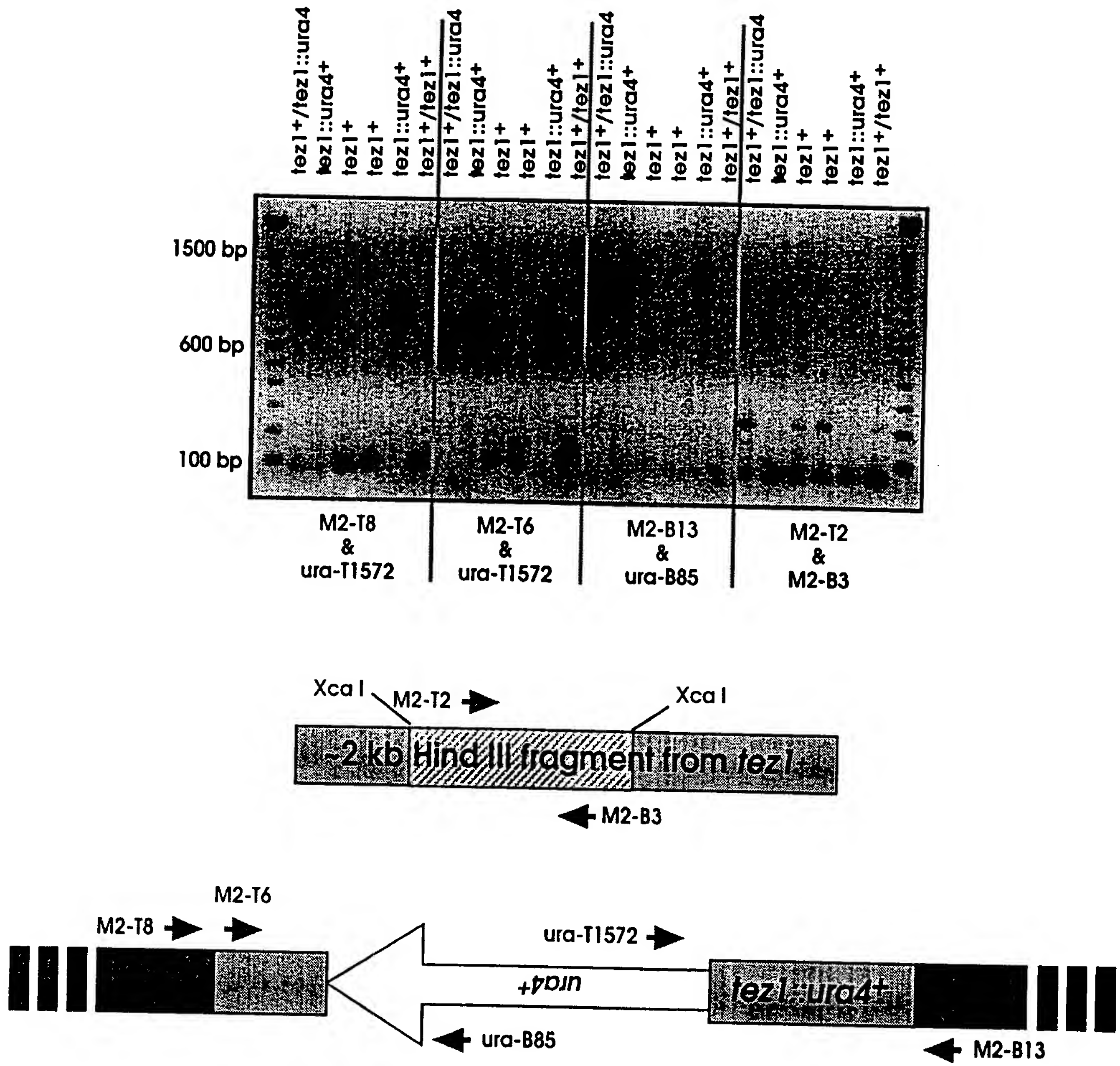


FIGURE 45

Tez1 disruption causes progressive shortening of telomeres in *S. pombe*

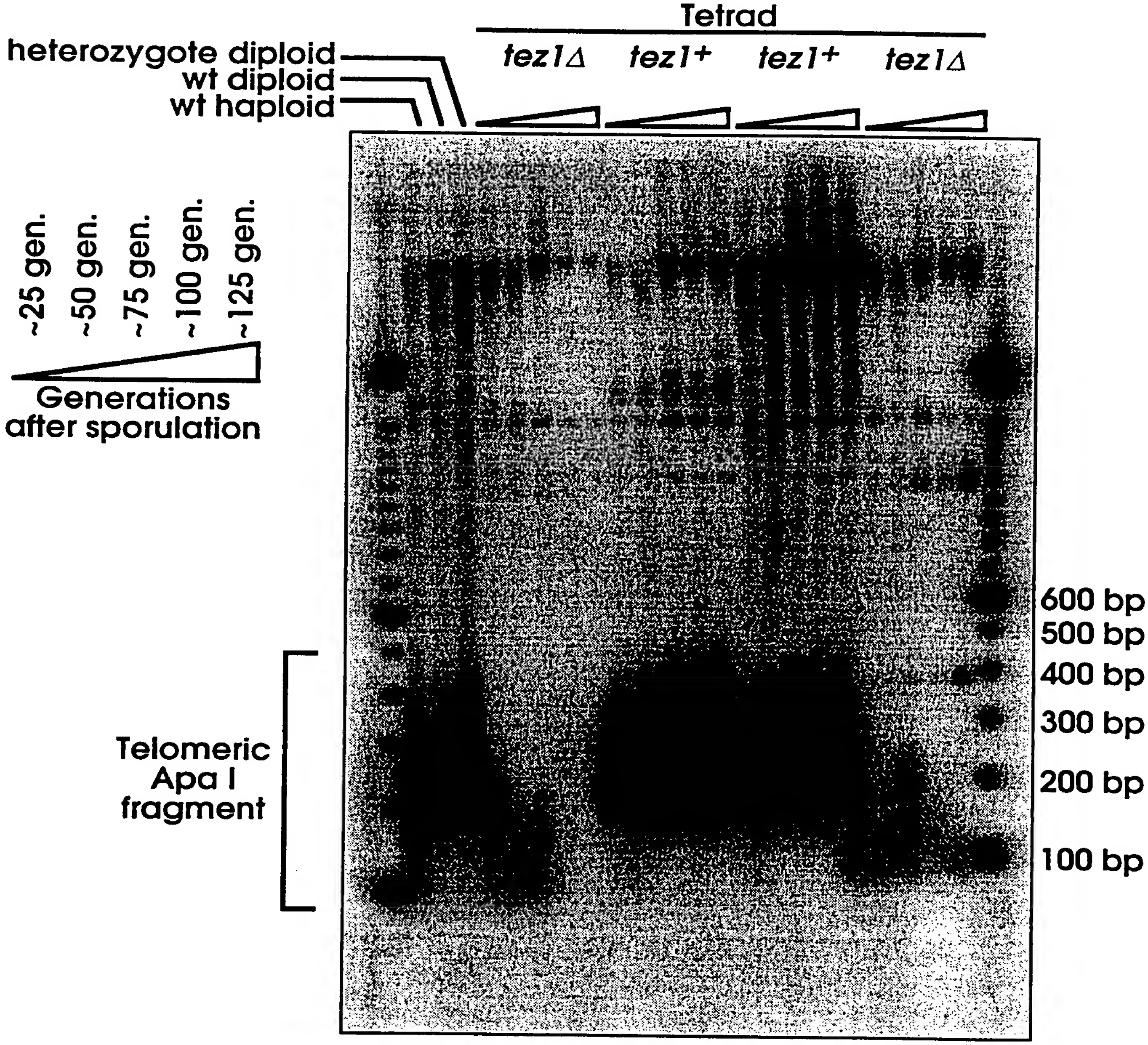


FIGURE 46

```
1 ggtaccgatttactttcctttcttcataagctaattgcttcctcgaacgctcctaaatctctggaaatatttttacaaga 80
81 actcaataacaataccaagtcaaattccaatatgaaggtgttattagtgatcgataatatttctattttatcggtcgtta 160
161 ccaagtataaggacaaaagaacaacttccttcccccctaaagacttttactttattaatttacttttcaaatatatttcg 240
241 ggttcgcttacttttaatcgtggtactgttttagctgctacttctagccaaccgcgtgtttctaccccgtcattggatat 320
321 agctcttggagtagctcacagaaatccttacaaatcttctgatgagactatattagattcattacagtccgtgcatattc 400
401 ttaacatggagccttacactttagatgagtcacgtcgcatgatggagtatttggtatcatccaacgtttgccttgaaaag 480
481 gttgataattatttgcaaaatcatgtccttagtggtggtaatccgcgaaagtttttttgatgcttgcacacgtctagcatg 560
561 attgagatattcaaaaatttctatccactacaactcctttaacgcggttttattttttctatttctattctcatgttgtt 640
641 ccaaatatgtatcatctcgtattaggcttttttccgtttactcctggaatcgtacctttttcactattccccctaatga 720
721 ataatctaaattagtttcgcttataattgatagtagtagaaagattggtgattctactcgtgtaatgttattagtttaaa 800
801 gatactttgcaaaacatttattagctatcattatataaaaaaaatcctataattataaatattaatcaatatttgcggtc 880
881 actatttatttaaaacgttatgatcagtaggacactttgcatatatatagttatgcttaatggttacttgtaacttgc    958

959 ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG AAT CAA TAT GTA   1018
  1 M   T   E   H   H   T   P   K   S   R   I   L   R   F   L   E   N   Q   Y   V     20

1019 TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT TTG AGA GGG TCG CCG GCA AGC TCG  1078
  21 Y   L   C   T   L   N   D   Y   V   Q   L   V   L   R   G   S   P   A   S   S    40

1079 TAT AGC AAT ATA TGC GAA CGC TTG AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT  1138
  41 Y   S   N   I   C   E   R   L   R   S   D   V   Q   T   S   F   S   I   F   L    60

1139 CAT TCG ACT GTA GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA  1198
  61 H   S   T   V   V   G   F   D   S   K   P   D   E   G   V   Q   F   S   S   P    80
```

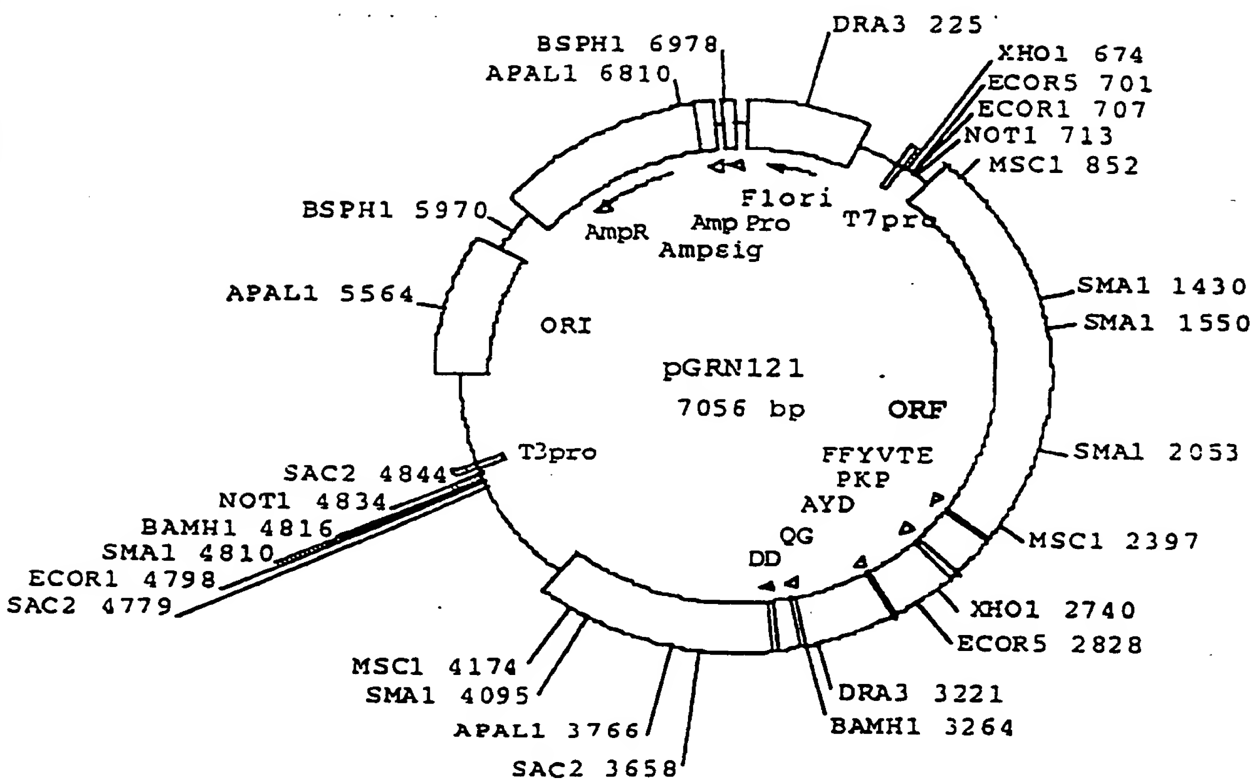
FIGURE 47

```
                                 1
                                met ser val tyr val val glu leu leu
GCCAAGTTCCTGCACTGGCTG           ATG AGT GTG TAC GTC GTC GAG CTG CTC

 10                                          20
arg ser phe phe tyr val thr glu thr thr phe gln lys asn arg
AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG

                         30
leu phe phe tyr arg lys ser val trp ser lys leu gln ser ile
CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT

 40                                          50
gly ile arg gln his leu lys arg val gln leu arg glu leu ser
GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG TCG

                         60
glu ala glu val arg gln his arg glu ala arg pro ala leu leu
GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG CTG

 70                                          80
thr ser arg leu arg phe ile pro lys pro asp gly leu arg pro
ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG CCG

                         90
ile val asn met asp tyr val val gly ala arg thr phe arg arg
ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC AGA

100                                         110
glu lys     ala glu arg leu thr ser arg val lys ala leu phe
GAA AAG ARG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG TTC

                        120
ser val leu asn tyr glu arg ala arg arg pro gly leu leu gly
AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG GGC

130                                         140
ala ser val leu gly leu asp asp ile his arg ala trp arg thr
GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC ACC

                        150
phe val leu arg val arg ala gln asp pro pro pro glu leu tyr
TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG TAC

160                                         170
phe val lys val asp val thr gly ala tyr asp thr ile pro gln
TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC CAG

                        180
asp arg leu thr glu val ile ala ser ile ile lys pro gln asn
GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC
```

FIGURE 48

```
Motif -1
Ep p123      ...LVVSLIRCFFYVTEQQKSYSKT...
Sp Tez1      ...FIIPILQSFFYITESSDLRNRT...
Sc Est2      ...LIPKIIQTFFYCTEISSTVTIV...
Hs TCP1      ...YVVELLRSFFYVTETTFQKNRL...
consensus          FFY TE

                          K
Motif 0          p hhh  K     hR h       R
Ep p123      ...KSLGFAPGKLRLIPKKT--TFRPIMTFNKKIV...
Sp Tez1      ...QKTTLPPAVIRLLPKKN--TFRLITNLRKRFL...
Sc Est2      ...TLSNFNHSKMRIIPKKSNNEFRIIAIPCRGAD...
Hs TCP1      ...ARPALLTSRLRFIPKPD--GLRPIVNMDYVVG...
consensus           R  PK      R I

               AF
Motif A       h  hDh  GY  h
Ep p123      ...PKLFFATMDIEKCYDSVNREKLSTFLK...
Sp Tez1      ...RKKYFVRIDIKSCYDRIKQDLMFRIVK...
Sc Est2      ...PELYFMKFDVKSCYDSIPRMECMRILK...
Hs TCP1      ...PELYFVKVDVTGAYDTIPQDRLTEVIA...//...
consensus        F   D    YD

Motif B            hPQG   pS hh
Ep p123      ...NGKFYKQTKGIPQGLCVSSILSSFYYA...
Sp Tez1      ...GNSQYLQKVGIPQGSILSSFLCHFYME...
Sc Est2      ...EDKCYIREDGLFQGSSLSAPIVDLVYD...
Hs TCP1      ...RATSYVQCQGIPQGSILSTLLCSLCYG...
consensus            G  QG    S

              Y
Motif C        h   F DDhhh
Ep p123      ...PNVNLLMRLTDDYLLITTQENN...

Sp Tez1      ...KKGSVLLRVVDDFLFITVNKKD...
Sc Est2      ...SQDTLILKLADDFLIISTDQQQ...
Hs TCP1      ...RRDGLLLRLVDDFLLVTPHLTH...
consensus              DD L

Motif D         Gh h  cK
Ep p123      ...NVSRENGFKFNMKKL...
Sp Tez1      ...LNLSLRGFEKHNFST...
Sc Est2      ...KKLAMGGFQKYNAKA...
Hs TCP1      ...LRTLVRGVPEYGCVV...
consensus         G
```

FIGURE 49



DRA3 225
XHO1 674
ECOR5 701
ECOR1 707
NOT1 713
MSC1 852
SMA1 1430
SMA1 1550
SMA1 2053
MSC1 2397
XHO1 2740
ECOR5 2828
DRA3 3221
BAMH1 3264
SAC2 3658
APAL1 3766
SMA1 4095
MSC1 4174
SAC2 4779
ECOR1 4798
SMA1 4810
BAMH1 4816
NOT1 4834
SAC2 4844
APAL1 5564
BSPH1 5970
APAL1 6810
BSPH1 6978
F1ori
T7pro
Amp Pro
AmpR
Ampsig
ORI
pGRN121
7056 bp
ORF
FFYVTE
PKP
AYD
QG
DD
T3pro

FIGURE 50

1 GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC
51 CCGCGATGCC GCGCGCTCCC CGCTGCCGAG CCGTGCGCTC CCTGCTGCGC
101 AGCCACTACC GCGAGGTGCT GCCGCTGGCC ACGTTCGTGC GGCGCCTGGG
151 GCCCCAGGGC TGGCGGCTGG TGCAGCGCGG GGACCCGGCG GCTTTCCGCG
201 CGNTGGTGGC CCANTGCNTG GTGTGCGTGC CCTGGGANGN ANGGCNGCCC
251 CCCGCCGCCC CCTCCTTCCG CCAGGTGTCC TGCCTGAANG ANCTGGTGGC
301 CCGAGTGCTG CANANGCTGT GCGANCGCGG CGCGAANAAC GTGCTGGCCT
351 TCGGCTTCGC GCTGCTGGAC GGGGCCCGCG GGGGCCCCCC CGAGGCCTTC
401 ACCACCAGCG TGCGCAGCTA CCTGCCCAAC ACGGTGACCG ACGCACTGCG
451 GGGGAGCGGG GCGTGGGGGC TGCTGCTGCG CCGCGTGGGC GACGACGTGC
501 TGGTTCACCT GCTGGCACGC TGCGCGNTNT TTGTGCTGGT GGNTCCCAGC
551 TGCGCCTACC ANGTGTGCGG GCCGCCGCTG TACCAGCTCG GCGCTGCNAC
601 TCAGGCCCGG CCCCCGCCAC ACGCTANTGG ACCCGAANGC GTCTGGGATC
651 CAACGGGCCT GGAACCATAG CGTCAGGGAG GCCGGGGTCC CCCTGGGCTG
701 CCAGCCCCGG GTGCGAGGAG GCGCGGGGGC AGTGCCAGCC GAAGTCTGCC
751 GTTGCCCAAG AGGCCCAGGC GTGGCGCTGC CCCTGAGCCG GAGCGGACGC
801 CCGTTGGGCA GGGGTCCTGG GCCCACCCGG GCAGGACGCC TGGACCGAGT
851 GACCGTGGTT TCTGTGTGGT GTCACCTGCC AGACCCGCCG AAGAAGCCAC
901 CTCTTTGGAG GGTGCGCTCT CTGGCACGCG CCACTCCCAC CCATCCGTGG
951 GCCGCCAGCA CCACGCGGGC CCCCCATCCA CATCGCGGCC ACCACGTCCT
1001 GGGACACGCC TTGTCCCCCG GTGTACGCCG AGACCAAGCA CTTCCTCTAC
1051 TCCTCAGGCG ACAAGNACAC TGCGNCCCTC CTTCCTACTC AATATATCTG
1101 AGGCCCAGCC TGACTGGCGT TCGGGAGGTT CGTGGAGACA NTCTTTCTGG
1151 TTCCAGGCCT TGGATGCCAG GATTCCCCGC AGGTTGCCCC GCCTGCCCCA
1201 GCGNTACTGG CAAATGCGGC CCCTGTTTCT GGAGCTGCTT GGGAACCACG
1251 CGCAGTGCCC CTACGGGGTG TTCCTCAAGA CGCACTGCCC GCTGCGAGCT
1301 GCGGTCACCC CAGCAGCCGG TGTCTGTGCC CGGGAGAAGC CCCAGGGCTC
1351 TGTGGCGGCC CCCGAGGAGG AGGAACACAG ACCCCCGTCG CCTGGTGCAG
1401 CTGCTCCGCC AGCACAGCAG CCCCTGGCAG GTGTACGGCT TCGTGCGGGC
1451 CTGCCTGCGC CGGCTGGTGC CCCCAGGCCT CTGGGGCTCC AGGCACAACG
1501 AACGCCGCTT CCTCAGGAAC ACCAAGAAGT TCATCTCCCT GGGGAAGCAT
1551 GCCAAGCTCT CGCTGCAGGA GCTGACGTGG AAGATGAGCG TGCGGGACTG
1601 CGCTTGGCTG CGCAGGAGCC CAGGGGTTGG CTGTGTTCCG GCCGCAGAGC
1651 ACCGTCTGCG TGAGGAGATC CTGGCCAAGT TCCTGCACTG GCTGATGAGT
1701 GTGTACGTCG TCGAGCTGCT CAGGTCTTTC TTTTATGTCA CGGAGACCAC
1751 GTTTCAAAAG AACAGGCTCT TTTTCTACCG GAAGAGTGTC TGGAGCAAGT
1801 TGCAAAGCAT TGGAATCAGA CAGCACTTGA AGAGGGTGCA GCTGCGGGAG
1851 CTGTCGGAAG CAGAGGTCAG GCAGCATCGG GAAGCCAGGC CCGCCCTGCT
1901 GACGTCCAGA CTCCGCTTCA TCCCCAAGCC TGACGGGCTG CGGCCGATTG
1951 TGAACATGGA CTACGTCGTG GGAGCCAGAA CGTTCCGCAG AGAAAAGAGG
2001 GCCGAGCGTC TCACCTCGAG GGTGAAGGCA CTGTTCAGCG TGCTCAACTA
2051 CGAGCGGGCG CGGCGCCCCG GCCTCCTGGG CGCCTCTGTG CTGGGCCTGG
2101 ACGATATCCA CAGGGCCTGG CGCACCTTCG TGCTGCGTGT GCGGGCCCAG
2151 GACCCGCCGC CTGAGCTGTA CTTTGTCAAG GTGGATGTGA CGGGCGCGTA
2201 CGACACCATC CCCCAGGACA GGCTCACGGA GGTCATCGCC AGCATCATCA
2251 AACCCCAGAA CACGTACTGC GTGCGTCGGT ATGCCGTGGT CCAGAAGGCC

FIGURE 51

```
      GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTTGCCCCGGCCACCCCCGCGATGCC
    1 ---------+---------+---------+---------+---------+---------+ 60
      CGTCGCGACGCAGGACGACGCGTGCACCCTTCGGGAACGGGGCCGGTGGGGGCGCTACGG

a     A  A  L  R  P  A  A  H  V  G  S  P  C  P  G  H  P  R  D  A  -
b      Q  R  C  V  L  L  R  T  W  E  A  L  A  P  A  T  P  A  M  P  -
c       S  A  A  S  C  C  A  R  G  K  P  W  P  R  P  P  P  R  C  R -

      GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT
   61 ---------+---------+---------+---------+---------+---------+ 120
      CGCGCGAGGGGCGACGGCTCGGCACGCGAGGGACGACGCGTCGGTGATGGCGCTCCACGA

a     A  R  S  P  L  P  S  R  A  L  P  A  A  Q  P  L  P  R  G  A  -
b      R  A  P  R  C  R  A  V  R  S  L  L  R  S  H  Y  R  E  V  L  -
c       A  L  P  A  A  E  P  C  A  P  C  C  A  A  T  T  A  R  C  C -

      GCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGG
  121 ---------+---------+---------+---------+---------+---------+ 180
      CGGCGACCGGTGCAAGCACGCCGCGGACCCCGGGGTCCCGACCGCCGACCACGTCGCGCC

a     A  A  G  H  V  R  A  A  P  G  A  P  G  L  A  A  G  A  A  R  -
b      P  L  A  T  F  V  R  R  L  G  P  Q  G  W  R  L  V  Q  R  G  -
c       R  W  P  R  S  C  G  A  W  G  P  R  A  G  G  W  C  S  A  G -

      GGACCCGGCGGCTTTCCGCGCCGNTGGTGGCCCANTGCNTGGTGTGCCGTGCCCTGGGANGN
  181 ---------+---------+---------+---------+---------+---------+ 240
      CCTGGGCCGCCGAAAGGCGCGCNACCACCGGGTNACGNACCACACGCACGGCACCCTNCN

a     G  P  G  G  F  P  R  ?  G  G  P  ?  ?  G  V  R  A  L  G  ?  -
b      D  P  A  A  F  R  A  ?  V  A  ?  C  ?  V  C  V  P  W  ?  ?  -
c       T  R  R  L  S  A  R  W  W  P  ?  A  W  C  A  C  P  G  ?  ? -

      ANGGCNGCCCCTCCGCTGCCCCCTCCTTCCGCCAGGTGTCCTGCCTGAANGANCTGGTGGC
  241 ---------+---------+---------+---------+---------+---------+ 300
      TNCCGNCGGGGAGGCGACGGGGGAGGAAGGCGGTCCACAGGACGGACTTNCTNGACCACCG

a     ?  A  A  P  R  R  P  L  L  P  P  G  V  L  P  E  ?  ?  G  G  -
b      ?  ?  P  P  A  A  P  S  P  R  Q  V  S  C  L  ?  ?  L  V  A  -
c       G  ?  P  P  P  P  P  P  S  A  R  C  P  A  *  ?  ?  W  W  P -

      CCGAGTGCTGCANANGCTGTGCGANCCCCCCCGAANAACGTGCTGGCCTTCGGCTTCGC
  301 ---------+---------+---------+---------+---------+---------+ 360
      GGCTCACGACGTNTNCGACACGCTNGGGCCGCGCTTNTTGCACGACCGGAAGCCGAAGCG

a     P  S  A  A  ?  A  V  R  ?  R  R  E  ?  R  A  G  L  R  L  R  -
b      P  V  L  ?  ?  L  C  ?  R  G  A  ?  N  V  L  A  F  G  F  A  -
c       E  C  C  ?  ?  C  A  ?  A  A  R  ?  T  C  W  P  S  A  S  R -

      GCTGCTGGACGGGGCCCGCGGGGGCCCCCCCGACCCCTTCACCACCAGCGTGCGCAGCTA
  361 ---------+---------+---------+---------+---------+---------+ 420
      CGACGACCTGCCCCGGGCGCCCCCGGGGGGGCTGGGGAAGTGGTGGTCGCACGCGTCGAT

a     A  A  G  R  G  P  R  G  P  P  R  G  L  H  H  Q  R  A  Q  L  -
b      L  L  D  G  A  R  G  G  P  P  E  A  P  T  T  S  V  R  S  Y  -
c       C  W  T  G  P  A  G  A  P  P  R  P  S  P  P  A  C  A  A  P -
```

FIGURE 51 (cont.)

```
      CCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCTGCG
  421 ---------+---------+---------+---------+---------+---------+ 490
      GGACGGGTTGTGCCACTGGCTGCGTGACGCCCCCTCGCCCCGCACCCCCGACGACGACGC

a     P  A  Q  H  G  D  R  R  T  A  G  E  R  G  V  G  A  A  A  A
b      L  P  N  T  V  T  D  A  L  R  G  S  G  A  W  G  L  L  L  K  -
c       C  P  T  R  *  P  T  H  C  G  G  A  G  R  G  G  C  C  C  A  -

      CCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCNTNTTTCTCCTGGT
  481 ---------+---------+---------+---------+---------+---------+ 540
      GGCGCACCCGCTGCTGCACGACCAAGTGGACGACCGTGCGACGCGCNANAAACACGACCA

a     P  R  C  R  R  R  A  G  S  P  A  G  T  L  R  ?  ?  C  A  G  -
b      K  V  G  D  D  V  L  V  H  L  L  A  R  C  A  ?  F  V  L  V  -
c       A  W  A  T  T  C  W  F  T  C  W  H  A  A  R  ?  L  C  W  W  .

      GGNTCCCACCTGCGGCTACCANGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCNAC
  541 ---------+---------+---------+---------+---------+---------+ 600
      CCNAGGGTGGACGCCGATGGTNCACACGCCCGGCGGCGACATGGTCGAGCCGCGACGNTG

a     G  S  Q  L  R  L  P  ?  V  R  A  A  A  V  P  A  R  R  C  ?  -
b      ?  P  S  C  A  Y  ?  V  C  G  P  P  L  Y  Q  L  G  A  A  T  -
c       ?  P  A  A  P  T  ?  C  A  G  R  R  C  T  S  S  A  L  ?  L  -

      TCAGGCCCGGCCCCCGCCACACCCTANTCCACCCCAANGCCTCTGGGATCCAACGGGCCT
  601 ---------+---------+---------+---------+---------+---------+ 660
      AGTCCGGGCCGGGGGCGGTGTGGGATNAGGTGGGGTTNCGGAGACCCTAGGTTGCCCGGA

a     S  C  P  A  P  A  T  R  ?  W  T  R  ?  R  L  G  S  N  G  P  -
b      Q  A  R  P  P  P  H  A  ?  G  P  E  ?  V  W  D  P  T  G  L  -
c       R  P  G  P  R  H  T  L  ?  D  P  ?  A  S  G  I  Q  R  A  W  .

      GGAACCATAGCGTCAGGGAGGCCGCCGTTCCCCCTGCCCTCCCAGCCCCGGGTGCCAGCAG
  661 ---------+---------+---------+---------+---------+---------+ 720
      CCTTGGTATCGCAGTCCCTCCGGCGGCAAGGGGGACGGGAGGGTCGGGGCCCACGGTCGTC

a     G  T  I  A  S  C  R  P  G  S  P  W  A  A  S  P  G  C  E  E  -
b      E  P  *  R  Q  G  G  R  C  P  P  G  L  P  A  P  G  A  R  R  -
c       N  H  S  V  R  E  A  G  V  P  L  G  C  Q  P  R  V  R  G  G  -

      GCGCCGGGCCAGTGGCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGC
  721 ---------+---------+---------+---------+---------+---------+ 780
      CGCGGCCCGGTCACCGTCGGCTTCAGACGGCAACGGGTTCTCCGGGTCCGCACCGCGACG

a     A  R  G  Q  C  Q  P  K  S  A  V  A  Q  E  A  Q  A  W  R  C
b      R  G  G  S  A  S  R  S  L  P  L  P  K  R  P  R  R  G  A  A  .
c       A  G  A  V  P  A  E  V  C  R  C  P  R  G  P  G  V  A  L  ?  -

      CCCTGAGCCGGACGCGACCCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCT
  781 ---------+---------+---------+---------+---------+---------+ 840
      GGGACTCGGCCTGCGCTGGGGGCAACCCGTCCCCAGGACCCGGGTGGGCCCGTCCTGCGA

a     P  *  A  C  A  D  A  R  W  A  C  V  L  G  P  P  G  Q  D  A  -
b      P  E  P  E  R  T  P  V  G  Q  G  S  W  A  H  P  G  R  T  ?  -
c       L  S  R  S  G  R  P  L  G  R  G  P  G  P  T  R  A  C  R  ?  -
```

FIGURE 52

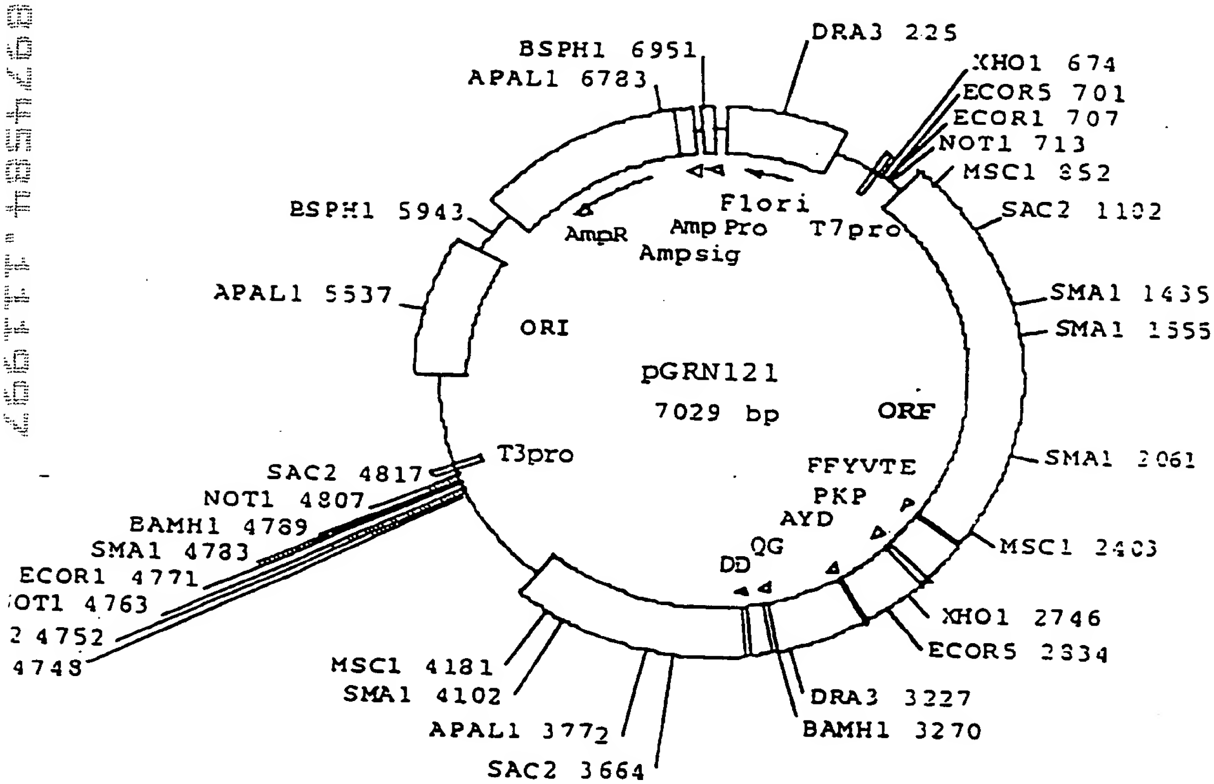

DRA3 225
XHO1 674
ECOR5 701
ECOR1 707
NOT1 713
MSC1 852
SAC2 1102
SMA1 1435
SMA1 1555
SMA1 2061
MSC1 2403
XHO1 2746
ECOR5 2334
DRA3 3227
BAMH1 3270
SAC2 3664
APAL1 3772
SMA1 4102
MSC1 4181
4748
2 4752
OT1 4763
ECOR1 4771
SMA1 4783
BAMH1 4789
NOT1 4807
SAC2 4817
APAL1 5537
BSPH1 5943
APAL1 6783
BSPH1 6951
Flori
Amp Pro
T7pro
AmpR
Ampsig
ORI
pGRN121
7029 bp
ORF
T3pro
FFYVTE
PKP
AYD
QG
DD
P

FIGURE 53

1
met
GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG

10
pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

20 30
his tyr arg glu val leu pro leu ala thr phe val arg arg leu
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

40
gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

50 60
phe arg ala leu val ala gln cys leu val cys val pro trp asp
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

70
ala arg pro pro pro ala ala pro ser phe arg gln val ser cys
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

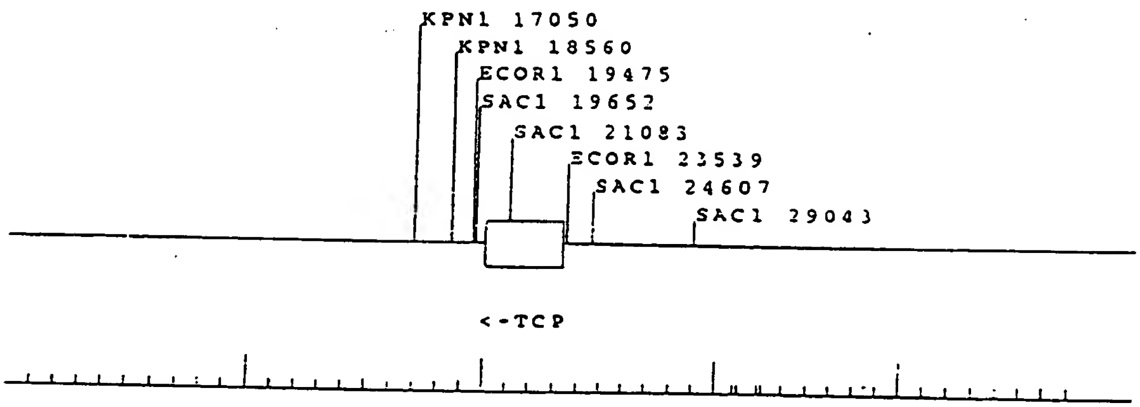
80 90
leu lys glu leu val ala arg val leu gln arg leu cys glu arg
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

100
gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

110 120
ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

130
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

FIGURE 54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KPN1 18560
ECOR1 19475
SAC1 19652
SAC1 21083
ECOR1 23539
SAC1 24607
SAC1 29043
<-TCP

```
                              Motif T
TRT con              WL     hh hh pFFY TE p    p    Y R    W  L  h I     K
Sp_Trt1p  429  WLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIWKLLCRPFITSMKM   8
hTRT      546  WLMSVYVVELLRSFFYVTETTFQKNRLPFYRPSVWSKLQSIGIRQHLK  10
Ea_p123   441  WIPEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSIADLKK   8
Sc_Est2p  366  WLPRQLIPKIIQTFFYCTEISSTVT-IVYFRHDTWNKLITPFIVEYFK   8


                          Motif 1        Motif 2                                        Motif A
TRT con                h     hRhIPKK p     FRhI .h   h        K             PcLYFh hDh  CYD I        hhK   K
Sp_Trt1p   NNVRMDTQKTTLPPAVIRLLPKKNT- 0 FRLITNLRKRFLIKMGSNKKMLVSTNQTL 40 PGRKKYFVRIDIKSCYDRIKQDLMFRIVKKKLKD   82
hTRT       EVRQHREARPALLTSRLRFIPKPDG- 0 LRPIVNMDYVVGARTFRREKRAERLTSRV 45 PPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKP   87
Ea_p123    KEVEEWKKSLGFAPGKLRLIPKKTT- 0 FRPIMTFNKKIVNSDRKTTKLTTNTKLLN 41 GQPKLFFATMDIEKCYDSVNREKLSTFLKTTKLL 100
Sc_Est2p   CRNHNSYTLSNFNHSKMRIIPKKSNN 1 FRIIAIPCRGADEEEFTIYKENHKNAIQP 42 VLPELYFMKFDVKSCYDSIPRMECMRILKDALKN  68
                                                    R                          AF
RT con                 p hh  h K       hR h         K                 h  hDh   GY  h
Sc_a1      LSNELGTGKFKFKPMRIVNIPKPKGG 0 IRPLSVGNPRDKIVQEVMRMILDTIFDKK 27 PGGSNWFIEVDLKKCFDTISHDLIIKELKRYISD   20
Bm_R1      RCVVEGTPPPVWKDGRLLVLPKGNGR 7 YRPVTLLPVLGKILEKVLLQCAPGLTHSI 24 EQRYVMAIFLDISGAFDNAWWPHIMVKAKRNCPP   23
HIV-1      EGKISKIGPENPYNTPVFAIKKKDST 1 WRKLVDFRELNKRTQDFWEVQLGIPHPAG  0 LKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIP    7
                       ▲                  ▲                ▲


                   Motif B'                        Motif C                            Motif D           Motif E
TRT con    K Y Q  GIPQGS LS hL  h Y DL       F       LLRL DDFLhIT       A  F    h G  c p   N cK             W G S
Sp_Trt1p   SQYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFT  6 LLRVVDDFLFITVNKKD 0 AKKFLNLSLRGFEKHNFSTSLEKTVI 17 KKRMPFFGFSV 181
hTRT       KSYVQCQGIPQGSILSTLLCSLCYGDMENKLFAGI  5 LLRLVDDFLLVTPHLTH 0 AKTFLRTLVRGVPEYGCVVNLRKTVV 19 HGLFPWCGLLL 197
Ea_p123    KFYKQTKGIPQGLCVSSILSSFYYATLEESSLGFL 14 LMRLTDDYLLITTQENN 0 AVLFIEKLINVSRENGFKFNMKKLQT 23 QDYCDWIGISI 179
Sc_Est2p   KCYIREDGLFQGSSLSAPIVDLVYDDLLEFYSEFK  8 ILKLADDFLIISTDQQQ 0 VINIKKLAMGGFQKYNAKANRDKILA 20 KELEVWKHSST 146
                                                        F
RT con             hPQG   pP hh   h                h  Y DDhhh                      Gh h  cK  h          hLG  h
Sc_a1      TYHKPMLGLPQGSLISPILCNIVMTLVDNWLEDYI 55 YVRYADDILIGVLGSKN 2 KMIKRDLNNFLNS-LGLTMNEEKTLI  4 ETPARFLGYNI
Bm_R1      EWKVSTMGCPQGSVLGPTLWNVLMDDLLALPQGIE  3 MVAYADDVTVLVRGDSR 6 AHAVLGLAEGWASRNKLDFAPAKSRC 22 ENQVTVLGVSS
HIV-1      GIRYQYNVLPQGWKGSPAIFQSSMTKILEPFKKQN  4 IYQYMDDLYVGSDLEIG 1 HRTKIEELRQHLLRWGLTTPDKKHQK  0 EPPFLWMGITL
             ▲                                      ▲   ▲
```

FIG. 55

mTRT vs hTRT align.adj Formatted Alignment

```
hTCP1.2.aa.gw         VYVVELLRSF FYVTETTFQK NRLFFYRKSV WSKLQSIGIR QHLKRVQLRE   600
mTRT.1.aa.adj.gw      ---------- ---------- ---------- ---------- ----------
Consensus             .......... .......... .......... .......... ..........   600

hTCP1.2.aa.gw         LSEAEVRQHR EARPALL-TSRLRFIPKPDG LRPIVNMDYV VGARTFRREKR   649
mTRT.1.aa.adj.gw      ------SQHK QTLLAAMPISRLRHRPTKEN- WRPIVNMSYS MGARALGRRK    43
Consensus             ......QH.. ....A...S-RLRRFIPKP.. .RPIVNM.N. .GAR...R.K   650

hTCP1.2.aa.gw         RA----ERLT SRVKALFSVLNYERARRPGL LGASVLGLDDIHRAWRTFVL   695
mTRT.1.aa.adj.gw      QAQHFTQRL- ---KIIPESMLNYFPE----- --------FDVI-------KL    69
Consensus             .A.....RE. ...K.IPS.L.NYE........ .........DVI.........L   700

hTCP1.2.aa.gw         RVRAQDPPPE LYFVKVDVTG AYDTIPQDRL TEVIASIIKP QNTYCVRRYA   745
mTRT.1.aa.adj.gw      IDIAQSTSRG ---------- ---------- ---------- ----------    79
Consensus             ...AQ..... .......... .......... .......... ..........   750

hTCP1.2.aa.gw         VVQKAAHGHV RKAFKSHVST LTDLQPYMRQ FVAHLQETSP LRDAVVIEQS   795
mTRT.1.aa.adj.gw      ---------- ---------- ---------- ---------- ----------    79
Consensus             .......... .......... .......... .......... ..........   800

hTCP1.2.aa.gw         SSLNEASSGL FDVFLRFMCH HAVRIRGKSY VQCQGIPQGS ILSTLLCSLC   845
mTRT.1.aa.adj.gw      ---------- ---------- ---------- ---------- ----------    79
Consensus             .......... .......... .......... .......... ..........   850

hTCP1.2.aa.gw         YGDMENKLFA GIRRDGLLLR LVDDFLLVTP HLTHAKTFLR TLVRGVPEYG   895
mTRT.1.aa.adj.gw      ---------- ---------- ---------- ---------- ----------    79
Consensus             .......... .......... .......... .......... ..........   900

hTCP1.2.aa.gw         CVVNLRKTVV NFPVEDEALG GTAFVQMPAH GLFPWCGLLL DTRTLEVQSD   945
mTRT.1.aa.adj.gw      ---------- ---------- ---------- ---------- ----------    79
Consensus             .......... .......... .......... .......... ..........   950

hTCP1.2.aa.gw         YSSYARTSIR ASLTFNRGFK AGRNMRRKLF GVLRLKCHSL FLDLQVNSLQ   995
mTRT.1.aa.adj.gw      ---------- ---------- ---------- ---------- ----------    79
Consensus             .......... .......... .......... .......... ..........  1000

hTCP1.2.aa.gw         TVCTNIYKIL LLQAYRFHAC VLQLPFHQQV WKNPTFFLRV ISDTASLCYS  1045
mTRT.1.aa.adj.gw      ---------- ---------- ---------- ---------- ----------    79
Consensus             .......... .......... .......... .......... ..........  1050

hTCP1.2.aa.gw         ILKAKNAGMS LGAKGAAGPL PSEAVQWLCH QAFLLKLTRH RVTYVPLLGS  1095
mTRT.1.aa.adj.gw      ---------- ---------- ---------- ---------- ----------    79
Consensus             .......... .......... .......... .......... ..........  1100
```

FIG. 56 (1/2)

Telomerase Spectific Motifs

```
Motif                          MOTIF T
TRT con          W1               FFY TE                 y Rk  W  1     I     MOTIF T'
hTRT      546 WLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGI 13  E  V
spTRT     429 WLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIWKLLCRPFI 12 EAEVR
eaTRT     441 WIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSI 12 ENNVR
scTRT     366 WLFRQLIPKIIQTFFYCTEISSTVT.IVYFRHDTWNKLITPFI  9 EKEVE
                                                               ENNVC
```

FIG. 57A

FIGURE 58

```
                                                            1
                                                          met
GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG

                                     10
pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

             20                                      30
his tyr arg glu val leu pro leu ala thr phe val arg arg leu
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

                                     40
gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

             50                                      60
phe arg ala leu val ala gln cys leu val cys val pro trp asp
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

                                     70
ala arg pro pro pro ala ala pro ser phe arg gln val ser cys
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

             80                                      90
leu lys glu leu val ala arg val leu gln arg leu cys glu arg
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

                                    100
gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

            110                                     120
ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

                                    130
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG
```

FIGURE 59

(page 1 of 7 for Fig. 59: SEQ ID NO:122/123)

1
met
GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG
ATG

10
pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

20 30
his tyr arg glu val leu pro leu ala thr phe val arg arg leu
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

40
gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

50 60
phe arg ala leu val ala gln cys leu val cys val pro trp asp
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

70
ala arg pro pro pro ala ala pro ser phe arg gln val ser cys
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

80 90
leu lys glu leu val ala arg val leu gln arg leu cys glu arg
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

100
gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

110 120
ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

130
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

FIGURE 60
MOUSE TRT SEQUENCE

(SEQ ID NO:124; page 1 of 2)

```
1     CGGGTGGGAGGCCCATCCCGGCCTTGAGCACAATGACCCGCGCTCCTCGT
51    TGCCCCGCGGTGCGCTCTCTGCTGCGCAGCCGATACCGGGAGGTGTGGCC
101   GCTGGCAACCTTTGTGCGGCGCCTGGGGCCCGAGGGCAGGCGGCTTGTGC
151   AACCCGGGGACCCGAAGATCTACCGCACTTTGGTTGCCCAATGCCTAGTG
201   TGCATGCACTGGGGCTCACAGCCTCCACCTGCCGACCTTTCCTTCCACCA
251   GGTGTCATCCCTGAAAGAGCTGGTGGCCAGGGTTGTGCAGAGACTCTGCG
301   AGCGCAACGAGAGAAACGTGCTGGCTTTTGGCTTTGAGCTGCTTAACGAG
351   GCCAGAGGCGGGCCTCCCATGGCCTTCACTAGTAGCGTGCGTAGCTACTT
401   GCCCAACACTGTTATTGAGACCCTGCGTGTCAGTGGTGCATGGATGCTAC
451   TGTTGAGCCGAGTGGGCGACGACCTGCTGGTCTACCTGCTGGCACACTGT
501   GCTCTTTATCTTCTGGTGCCCCCCAGCTGTGCCTACCAGGTGTGTGGGTC
551   TCCCCTGTACCAAATTTGTGCCACCACGGATATCTGGCCCTCTGTGTCCG
601   CTAGTTACAGGCCCACCCGACCCGTGGGCAGGAATTTCACTAACCTTAGG
651   TTCTTACAACAGATCAAGAGCAGTAGTCGCCAGGAAGCACCGAAACCCCT
701   GGCCTTGCCATCTCGAGGTACAAAGAGGCATCTGAGTCTCACCAGTACAA
751   GTGTGCCTTCAGCTAAGAAGGCCAGATGCTATCCTGTCCCGAGAGTGGAG
801   GAGGGACCCCACAGGCAGGTGCTACCAACCCCATCAGGCAAATCATGGGT
851   GCCAAGTCCTGCTCGGTCCCCCGAGGTGCCTACTGCAGAGAAAGATTTGT
901   CTTCTAAAGGAAAGGTGTCTGACCTGAGTCTCTCTGGGTCGGTGTGCTGT
951   AAACACAAGCCCAGCTCCACATCTCTGCTGTCACCACCCCGCCAAAATGC
1001  CTTTCAGCTCAGGCCATTTATTGAGACCAGACATTTCCTTTACTCCAGGG
1051  GAGATGGCCAAGAGCGTCTAAACCCCTCATTCCTACTCAGCAACCTCCAG
1101  CCTAACTTGACTGGGGCCAGGAGACTGGTGGAGATCATCTTTCTGGGCTC
1151  AAGGCCTAGGACATCAGGACCACTCTGCAGGACACACCGTCTATCGCGTC
1201  GATACTGGCAGATGCGGCCCCTGTTCCAACAGCTGCTGGTGAACCATGCA
1251  GAGTGCCAATATGTCAGACTCCTCAGGTCACATTGCAGGTTTCGAACAGC
1301  AAACCAACAGGTGACAGATGCCTTGAACACCAGCCCACCGCACCTCATGG
1351  ATTTGCTCCGCCTGCACAGCAGTCCCTGGCAGGTATATGGTTTTCTTCGG
1401  GCCTGTCTCTGCAAGGTGGTGTCTGCTAGTCTCTGGGGTACCAGGCACAA
1451  TGAGCGCCGCTTCTTTAAGAACTTAAAGAAGTTCATCTCGTTGGGGAAAT
1501  ACGGCAAGCTATCACTGCAGGAACTGATGTGGAAGATGAAAGTAGAGGAT
1551  TGCCACTGGCTCCGCAGCAGCCCGGGGAAGGACCGTGTCCCCGCTGCAGA
1601  GCACCGTCTGAGGGAGAGGATCCTGGCTACGTTCCTGTTCTGGCTGATGG
1651  ACACATACGTGGTACAGCTGCTTAGGTCATTCTTTTACATCACAGAGAGC
1701  ACATTCCAGAAGAACAGGCTCTTCTTCTACCGTAAGAGTGTGTGGAGCAA
1751  GCTGCAGAGCATTGGAGTCAGGCAACACCTTGAGAGAGTGCGGCTACGGG
1801  AGCTGTCACAAGAGGAGGTCAGGCATCACCAGGACACCTGGCTAGCCATG
1851  CCCATCTGCAGACTGCGCTTCATCCCCAAGCCCAACGGCCTGCGGCCCAT
1901  TGTGAACATGAGTTATAGCATGGGTACCAGAGCTTTGGGCAGAAGGAAGC
```

FIGURE 53 (cont.)

```
               140                                          150
trp gly leu leu leu arg arg val gly asp asp val leu val his
TGG GGG CTG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC

                                    160
leu leu ala arg cys ala leu phe val leu val ala pro ser cys
CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC

               170                                          180
ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala
GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC

                                    190
thr gln ala arg pro pro pro his ala ser gly pro arg arg arg
ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT

               200                                          210
leu gly cys glu arg ala trp asn his ser val arg glu ala gly
CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

                                    220
val pro leu gly leu pro ala pro gly ala arg arg arg gly gly
GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC

               230                                          240
ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly
AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC

                                    250
ala ala pro glu pro glu arg thr pro val gly gln gly ser trp
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG

               260                                          270
ala his pro gly arg thr arg gly pro ser asp arg gly phe cys
GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

                                    280
val val ser pro ala arg pro ala glu glu ala thr ser leu glu
GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG
```

FIGURE 53 (cont.)

290 300
gly ala leu ser gly thr arg his ser his pro ser val gly arg
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

310
gln his his ala gly pro pro ser thr ser arg pro pro arg pro
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

320 330
trp asp thr pro cys pro pro val tyr ala glu thr lys his phe
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

340
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

350 360
leu ser ser leu arg pro ser leu thr gly ala arg arg leu val
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

370
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

380 390
arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

400
leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

410 420
val leu leu lys thr his cys pro leu arg ala ala val thr pro
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA

430
ala ala gly val cys ala arg glu lys pro gln gly ser val ala
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

FIGURE 53 (cont.)

```
                440                                                   450
ala pro glu glu glu asp thr asp pro arg arg leu val gln leu
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

                                    460
leu arg gln his ser ser pro trp gln val tyr gly phe val arg
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

                470                                                   480
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

                                    490
his asn glu arg arg phe leu arg asn thr lys lys phe ile ser
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

                500                                                   510
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

                                    520
met ser val arg asp cys ala trp leu arg arg ser pro gly val
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

                530                                                   540
gly cys val pro ala ala glu his arg leu arg glu glu ile leu
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

                                    550
ala lys phe leu his trp leu met ser val tyr val val glu leu
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

                560                                                   570
leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

                                    580
arg leu phe phe tyr arg pro ser val trp ser lys leu gln ser
AGG CTC TTT TTC TAC CGG CCG AGT GTC TGG AGC AAG TTG CAA AGC

                590                                                   600
ile gly ile arg gln his leu lys arg val gln leu arg glu leu
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG
```

FIGURE 53 (cont.)

610
ser glu ala glu val arg gln his arg glu ala arg pro ala leu
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620 630
leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

640
pro ile val asn met asp tyr val val gly ala arg thr phe arg
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

650 660
arg glu lys arg ala glu arg leu thr ser arg val lys ala leu
AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

670
phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu
TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

680 690
gly ala ser val leu gly leu asp asp ile his arg ala trp arg
GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

700
thr phe val leu arg val arg ala gln asp pro pro pro glu leu
ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

710 720
tyr phe val lys val asp val thr gly ala tyr asp thr ile pro
TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

730
gln asp arg leu thr glu val ile ala ser ile ile lys pro gln
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

740 750
asn thr tyr cys val arg arg tyr ala val val gln lys ala ala
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

760
his gly his val arg lys ala phe lys ser his val ser thr leu
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG

FIGURE 53 (cont.)

```
                770                                          780
thr asp leu gln pro tyr met arg gln phe val ala his leu gln
ACA GAC CTC CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG

                                    790
glu thr ser pro leu arg asp ala val val ile glu gln ser ser
GAG ACC AGC CCG CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC

                800                                          810
ser leu asn glu ala ser ser gly leu phe asp val phe leu arg
TCC CTG AAT GAG GCC AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC

                                    820
phe met cys his his ala val arg ile arg gly lys ser tyr val
TTC ATG TGC CAC CAC GCC GTG CGC ATC AGG GGC AAG TCC TAC GTC

                830                                          840
gln cys gln gly ile pro gln gly ser ile leu ser thr leu leu
CAG TGC CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC

                                    850
cys ser leu cys tyr gly asp met glu asn lys leu phe ala gly
TGC AGC CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG

                860                                          870
ile arg arg asp gly leu leu leu arg leu val asp asp phe leu
ATT CGG CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG

                                    880
leu val thr pro his leu thr his ala lys thr phe leu arg thr
TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC

                890                                          900
leu val arg gly val pro glu tyr gly cys val val asn leu arg
CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG

                                    910
lys thr val val asn phe pro val glu asp glu ala leu gly gly
AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC

                920                                          930
thr ala phe val gln met pro ala his gly leu phe pro trp cys
ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC
```

FIGURE 53 (cont.)

940
gly leu leu leu asp thr arg thr leu glu val gln ser asp tyr
GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC

950 960
ser ser tyr ala arg thr ser ile arg ala ser val thr phe asn
TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT GTC ACC TTC AAC

970
arg gly phe lys ala gly arg asn met arg arg lys leu phe gly
CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG

980 990
val leu arg leu lys cys his ser leu phe leu asp leu gln val
GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG

1000
asn ser leu gln thr val cys thr asn ile tyr lys ile leu leu
AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG

1010 1020
leu gln ala tyr arg phe his ala cys val leu gln leu pro phe
CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT

1030
his gln gln val trp lys asn pro thr phe phe leu arg val ile
CAT CAG CAA GTT TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC

1040 1050
ser asp thr ala ser leu cys tyr ser ile leu lys ala lys asn
TCT GAC ACG GCC TCC CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC

1060
ala gly met ser leu gly ala lys gly ala ala gly pro leu pro
GCA GGG ATG TCG CTG GGG GCC AAG GGC GCC GCC GGC CCT CTG CCC

1070 1080
ser glu ala val gln trp leu cys his gln ala phe leu leu lys
TCC GAG GCC GTG CAG TGG CTG TGC CAC CAA GCA TTC CTG CTC AAG

1090
leu thr arg his arg val thr tyr val pro leu leu gly ser leu
CTG ACT CGA CAC CGT GTC ACC TAC GTG CCA CTC CTG GGG TCA CTC

FIGURE 53 (cont.)

1100 1110
arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr
AGG ACA GCC CAG ACG CAG CTG AGT CGG AAG CTC CCG GGG ACG ACG

1120
leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp
CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG GCA CTG CCC TCA GAC

1130 1132
phe lys thr ile leu asp OP
TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCCACAGCCAGGCCGAGAGCAGA

CACCAGCAGCCCTGTCACGCCGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCCACACCC

AGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCC

GGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTC

CAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAG

CTTTTCYTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATT

CGCCATTGTTCACCCYTCGCCCTGCCYTCCTTTGCCTTCCACCCCCACCATCCAGGTGGA

GACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTA

CACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGAGGTGC

TGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGRAAAAAAAAAAAAAAAAAA

AAAAAAAAAA

FIGURE 51 (cont.)

```
        ACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGAGGGCCCAGGACCCGCCCC
   2101 ---------+---------+---------+---------+---------+---------+ 2160
        TGCTATAGGTGTCCCGGACCGCGTGGAAGCACGACGCACACTCCCGGGTCCTGGGCGGGG

a        T  I  S  T  C  P  G  A  P  S  C  C  V  C  G  F  R  T  R  R  -
b         R  Y  P  Q  G  L  A  H  L  R  A  A  C  A  G  P  G  P  A  A -
c          D  I  H  R  A  W  R  T  F  V  L  R  V  R  A  Q  D  P  P  P -

        CTCAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCAGGACA
   2161 ---------+---------+---------+---------+---------+---------+ 2220
        GAGTCGACATGAAACAGTTCCACCTACACTGCCCGCGCATGCTGTGGTAGGGGGTCCTGT

a        L  S  C  T  L  S  R  W  M  *  R  A  R  T  T  P  S  F  R  T  -
b         *  A  V  L  C  Q  G  G  C  D  G  R  V  R  H  H  P  P  G  Q
c          E  L  Y  F  V  K  V  D  V  T  G  A  Y  D  T  I  P  Q  D  K -

        GGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCGTCGGT
   2221 ---------+---------+---------+---------+---------+---------+ 2280
        CCGAGTGCCTCCAGTAGCGGTCGTAGTAGTTTGGGGTCTTGTGCATGACGCACGCAGCCA

a        G  S  R  R  S  S  P  A  S  S  N  P  R  T  R  T  A  C  V  G  -
b         A  H  G  G  H  R  Q  H  H  Q  T  P  E  H  V  L  R  A  S  V -
c          L  T  E  V  I  A  S  I  I  K  P  Q  N  T  Y  C  V  R  R  Y -

        ATGCCGTGGTCCAGAAGGCCCCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCT
   2281 ---------+---------+---------+---------+---------+---------+ 2340
        TACGGCACCAGGTCTTCCGGGGGGTACCCGTGCAGGCGTTCCGGAAGTTCTCGGTGCAGA

a        M  P  W  S  R  R  P  P  M  G  T  S  A  R  P  S  R  A  T  S  -
b         C  R  G  P  E  G  R  P  W  A  R  P  Q  G  L  Q  E  P  R  L -
c          A  V  V  Q  K  A  A  H  G  H  V  R  K  A  F  K  S  H  V  S

        CTACCTTGACAGACCTCCAGCCCTACATGCGACAGTTCGTGGCTCACCTGCAGGANAACA
   2341 ---------+---------+---------+---------+---------+---------+ 2400
        GATGGAACTGTCTGGAGGTCGGGATGTACGCTGTCAAGCACCGAGTGGACGTCCTNTTGT

a        L  P  *  Q  T  S  S  R  T  C  D  S  S  W  L  T  C  R  ?  T  -
b         Y  L  D  R  P  P  A  V  H  A  T  V  R  G  S  P  A  G  ?  Q -
c          T  L  T  D  L  Q  P  Y  M  R  Q  F  V  A  H  L  Q  ?  N  S -

        GCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTG
   2401 ---------+---------+---------+---------+---------+---------+ 2460
        CGGGCGACTCCCTACGGCAGCAGTAGCTCGTCTCGAGGAGGGACTTACTCCGGTCGTCAC

a        A  R  *  G  M  P  S  S  S  S  R  A  P  P  *  M  R  P  A  V  -
b         P  A  E  G  C  R  R  H  R  A  E  L  L  P  E  *  G  Q  Q  W -
c          P  L  R  D  A  V  V  I  E  Q  S  S  S  L  N  E  A  S  S  G -

        GCCTCTTCGACCTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGT
   2461 ---------+---------+---------+---------+---------+---------+ 2520
        CGGAGAAGCTGGAGAAGGATGCGAAGTACACGGTGGTGCGGCACGCGTAGTCCCCGTTCA

a        A  S  S  T  S  S  Y  A  S  C  A  T  T  P  C  A  S  G  A  S  -
b         P  L  R  R  L  P  T  L  H  V  P  P  R  R  A  H  Q  G  Q  V -
c          L  F  D  V  F  L  R  F  M  C  H  H  A  V  R  T  R  G  K  S -
```

FIGURE 51 (cont.)

```
       CCTACCTCCAGTGCCAGCGGATCCCCCAGGCCTCCATCCTCTCCACCTGCTCTGCAGCC
2521 ---------+---------+---------+---------+---------+---------+ 2580
       GGATGGAGGTCACGGTCCCCTAGGGCGTCCGGAGGTAGGAGAGGTGGACGAGACGTCGG

a      P  T  S  S  A  R  G  S  R  R  A  F  S  S  P  R  C  S  A  A  -
b       L  R  P  V  P  G  D  P  A  G  L  H  P  L  H  A  A  L  Q  P  -
c        Y  V  Q  C  Q  C  I  P  Q  G  S  I  L  S  T  L  L  C  S  L  -

       TGTACTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCC
2581 ---------+---------+---------+---------+---------+---------+ 2640
       ACATGATGCCGCTGTACCTCTTGTTCGACAAACGCCCCTAAGCCGCCCTGCCCGACGAGG

a      C  A  T  A  T  W  K  T  S  C  L  R  C  F  G  G  T  C  C  S  -
b       V  L  R  R  H  G  E  Q  A  V  C  G  D  S  A  G  R  A  A  P  -
c        C  Y  G  D  M  E  N  K  L  F  A  G  I  R  R  D  G  L  L  L  -

       TGCGTTTGGTGGATGATTTCTTGTTGGTCACACCTCACCTCACCCACGCGAAAACCTTCC
2641 ---------+---------+---------+---------+---------+---------+ 2700
       ACGCAAACCACCTACTAAAGAACAACCAGTGTGGAGTGGAGTGGGTGCGCTTTTGGAAGG

a      C  V  W  W  M  I  S  C  W  *  H  L  T  S  P  T  R  K  P  S  -
b       A  F  G  G  *  F  L  V  G  D  T  S  P  H  P  R  E  N  L  P  -
c        R  L  V  D  D  F  L  L  V  T  P  H  L  T  H  A  K  T  F  L  -

       TCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAG
2701 ---------+---------+---------+---------+---------+---------+ 2760
       AGTCCTGGGACCAGGCTCCACAGGGACTCATACCGACGCACCACTTGAACGCCTTCTGTC

a      S  G  P  W  S  E  V  S  L  S  M  A  A  W  *  T  C  G  R  Q  -
b       Q  D  P  G  P  R  C  P  *  V  W  L  R  G  E  L  A  E  D  S  -
c        P  T  L  V  R  G  V  P  E  Y  G  C  V  V  N  L  R  K  T  V  -

       TGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGG
2761 ---------+---------+---------+---------+---------+---------+ 2820
       ACCACTTGAAGGGACATCTTCTGCTCCGGGACCCACCGTGCCGAAAACAAGTCTACGGCC

a      W  *  T  S  L  *  K  T  R  P  W  V  A  R  L  L  F  R  C  H  -
b       G  E  L  P  C  R  R  R  G  P  C  W  H  G  F  C  S  D  A  G  -
c        V  N  F  P  V  E  D  E  A  L  G  G  T  A  F  V  Q  M  P  A  -

       CCCACGGCCTATTCCCCTCGTCCGCCCTGCTGCTCGATACCCGGACCCTCGAGGTCCAGA
2821 ---------+---------+---------+---------+---------+---------+ 2880
       GGGTGCCGGATAAGGGGAGCAGGCGGGACGACGAGCTATGGGCCTGGGACCTCCAGGTCT

a      P  T  A  Y  S  P  R  A  A  C  C  W  I  P  C  P  W  R  C  R  -
b       P  R  P  I  P  L  V  R  P  A  A  G  Y  P  D  P  G  G  A  E  -
c        H  G  L  F  P  W  C  G  L  L  L  D  T  R  T  L  E  V  Q  S  -

       GCGACTACTCCAGCTATGCCCGCACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCT
2881 ---------+---------+---------+---------+---------+---------+ 2940
       CGCTGATGAGGTCGATACGGGCGTGGAGGTAGTCTCGGTCAGAGTGGAAGTTGGCGCCGA

a      A  T  T  P  A  M  P  G  P  P  S  E  P  V  S  P  S  T  A  A  -
b       R  L  L  Q  L  C  P  D  L  H  Q  S  Q  S  H  L  Q  P  R  L  -
c        D  Y  S  S  Y  A  R  T  S  I  R  A  S  L  T  F  N  R  G  F  -
```

FIGURE 51 (cont.)

```
     TCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACA
2941 ---------+---------+---------+---------+---------+---------+ 3000
     AGTTCCGACCCTCCTTGTACGCAGCGTTTGAGAAACCCCAGAACGCCGACTTCACAGTGT

a     S  R  L  G  G  T  C  V  A  N  S  L  G  S  C  G  *  S  V  T
b      Q  G  W  E  E  H  A  S  Q  T  L  W  G  L  A  A  E  V  S  Q  -
c       K  A  G  R  N  M  R  R  K  L  F  G  V  L  R  L  K  C  H  S -

     GCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGA
3001 ---------+---------+---------+---------+---------+---------+ 3060
     CGGACAAAGACCTAAACGTCCACTTGTCGGAGGTCTGCCACACGTGGTTGTAGATGTTCT

a     A  C  F  W  I  C  R  *  T  A  S  R  R  C  A  P  T  S  T  R  -
b      P  V  S  G  F  A  G  E  Q  P  P  D  G  V  H  Q  H  L  Q  D  -
c       L  F  L  D  L  Q  V  N  S  L  Q  T  V  C  T  N  I  Y  K  I -

     TCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGC
3061 ---------+---------+---------+---------+---------+---------+ 3120
     AGGAGGACGACGTCCGCATGTCCAAAGTGCGTACACACGACGTCGAGGGTAAAGTAGTCG

a     S  S  C  C  R  R  T  G  F  T  H  V  C  C  S  S  H  F  I  S  -
b      P  P  A  A  G  V  Q  V  S  R  M  C  A  A  A  P  I  S  S  A -
c       L  L  L  Q  A  Y  R  F  H  A  C  V  L  Q  L  P  F  H  Q  Q -

     AAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCT
3121 ---------+---------+---------+---------+---------+---------+ 3180
     TTCAAACCTTCTTGGGGTGTAAAAAGGACGCGCAGTAGAGACTGTGCCGGAGGGAGACGA

a     K  F  G  R  T  P  H  F  S  C  A  S  S  L  T  R  P  P  S  A  -
b      S  L  E  E  P  H  I  F  P  A  R  H  L  *  H  G  L  P  L  L
c       V  W  K  N  P  T  F  F  L  R  V  I  S  D  T  A  S  L  C  Y

     ACTCCATCCTGAAAGCCAACAACGCAGGGATGTCGCTGGGGGCCAAGGGCGGCGCCCCCC
3181 ---------+---------+---------+---------+---------+---------+ 3240
     TGAGGTAGGACTTTCGGTTGTTGCGTCCCTACAGCGACCCCCGGTTCCCGCCGCGGGGGG

a     T  P  S  *  K  F  R  T  Q  G  C  R  W  G  P  R  A  F  P  A  -
b      L  H  P  E  S  Q  E  R  R  D  V  A  G  G  Q  G  R  R  R  P .
c       S  I  L  K  A  K  N  A  G  M  S  L  G  A  K  C  A  A  G  P -

     CTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTC
3241 ---------+---------+---------+---------+---------+---------+ 3300
     GAGACGGGAGGCTCCGGCACGTCACCGACACGGTGGTTCGTAAGGACGAGTTCGACTGAG

a     L  C  P  P  P  P  C  S  G  C  A  T  K  H  S  C  S  S  *  L  -
b      S  A  L  R  G  R  A  V  A  V  P  P  S  I  P  A  Q  A  D  S .
c       L  P  S  E  A  V  Q  W  L  C  H  Q  A  F  L  L  K  L  T  R -

     GACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGTTCAGACGCAGCTGA
3301 ---------+---------+---------+---------+---------+---------+ 3360
     CTGTGGCACAGTGGATGCACGGTGAGGACCCCAGTGAGTCCTGTCAAGTCTGCGTCGACT

a     D  T  V  S  P  T  C  H  S  W  G  H  S  G  Q  F  R  R  S  *  .
b      T  P  C  H  L  R  A  T  P  G  V  T  Q  D  S  P  D  A  A  E -
c       H  R  V  T  Y  V  S  L  L  G  S  L  R  T  A  Q  T  Q  L  S .
```

FIGURE 51 (cont.)

```
     GTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAACCCGGCACTGC
3361 ------------------------------------------------------------ 3420
     CAGCCTTCGAGGGCCCCTGCTGCGACTGACGGGACCTCCGGCGTCGGTTGGGCCGTGACG

a    V  G  S  S  R  G  R  R  *  L  P  W  R  P  Q  P  T  R  H  C   -
b     S  E  A  P  G  D  D  A  D  C  P  G  G  R  S  Q  P  G  T  A  -
c      R  K  L  P  G  T  T  L  T  A  L  E  A  A  A  N  P  A  L  P -

     CCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCCACAGCCAGGCCGAGAGCA
3421 ------------------------------------------------------------ 3480
     GGAGTCTGAAGTTCTGGTAGGACCTGACTACCGGTGGGCGGGTGTCGGTCCGGCTCTCGT

a    P  Q  T  S  R  P  S  W  T  D  G  H  P  P  T  A  R  P  R  A   -
b     L  R  L  Q  D  H  P  G  L  M  A  T  R  P  Q  P  G  R  E  Q  -
c      S  D  F  K  T  I  L  D  *  W  P  P  A  H  S  Q  A  E  S  R -

     GACACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCCACAC
3481 ------------------------------------------------------------ 3540
     CTGTGGTCGTCGGGACAGTGCGGCCCGAGATGCAGGGTCCCTCCCTCCCCGCCGGGTGTG

a    D  T  S  S  P  V  T  P  G  S  T  S  Q  G  G  R  G  G  P  H   -
b     T  P  A  A  L  S  R  R  A  L  R  P  R  E  G  G  A  A  H  T  -
c      H  Q  Q  P  C  H  A  G  L  Y  V  P  G  R  E  G  R  P  T  P -

     CCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGT
3541 ------------------------------------------------------------ 3600
     GGTCCGGGCGTGGCGACCCTCAGACTCCGGACTCACTCACAAACCGGCTCCGGACGTACA

a    P  G  P  H  R  W  E  S  E  A  *  V  S  V  W  P  R  P  A  C   -
b     Q  A  R  T  A  G  S  L  R  P  E  *  V  F  G  R  G  L  H  V  -
c      R  P  A  P  L  G  V  *  G  L  S  E  C  L  A  E  A  C  M  S -

     CCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGTGCTGAGTG
3601 ------------------------------------------------------------ 3660
     GGCCGACTTCCGACTCACAGGCCGACTCCGGACTCGCTCACAGGTCGGTTCACGACTCAC

a    P  A  E  G  *  V  S  G  *  G  L  S  E  C  P  A  K  C  *  V   -
b     R  L  K  A  E  C  P  A  E  A  *  A  S  V  Q  P  S  A  E  C  -
c      G  *  R  L  S  V  R  L  R  P  E  R  V  S  S  Q  V  L  S  V -

     TCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCC
3661 ------------------------------------------------------------ 3720
     AGGTCGTGTGGACGGCAGAAGTGAAGGGGTGTCCGACCGCGAGCCGAGGTGGGGTCCCGG

a    S  S  T  P  A  V  F  T  S  P  Q  A  G  A  R  L  H  P  R  A   -
b     P  A  H  L  P  S  S  L  P  H  R  L  A  L  G  S  T  P  G  P  -
c      Q  H  T  C  R  L  H  F  P  T  G  W  R  S  A  P  P  Q  G  Q -

     AGCTTTTCCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGA
3721 ------------------------------------------------------------ 3780
     TCGAAAAGGAGTGGTCCTCGGGCCGAAGGTGAGGGGTGTATCCTTATCAGGTAGGGGTCT

a    S  F  S  S  P  G  A  R  L  P  L  P  T  *  E  *  S  I  P  R
b     A  F  P  H  Q  E  P  G  F  H  S  P  H  R  N  S  P  S  P  D  -
c      L  F  L  T  R  S  P  A  S  T  P  H  I  G  I  V  H  P  Q  T -
```

FIGURE 51 (cont.)

```
       TTCGCCATTGTTCACCCCTCGCCCTGCCCTCCTTTGCCTTCCACCCCCACCATCCAGGTG
3781   ---------+---------+---------+---------+---------+---------+ 3840
       AAGCGGTAACAAGTGGGGAGCGGGACGGGAGGAAACGGAAGGTGGGGGTGGTAGGTCCAC

a      F  A  I  V  H  P  S  P  C  P  P  L  P  S  T  P  T  I  Q  V   -
b       S  P  L  F  T  P  R  P  A  L  L  C  L  P  P  P  P  S  R  W  -
c        R  H  C  S  P  L  A  L  P  S  F  A  F  H  P  H  H  P  G  G -

       GAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTG
3841   ---------+---------+---------+---------+---------+---------+ 3900
       CTCTGGGACTCTTCCTGGGACCCTCGAGACCCTTAAACCTCACTGGTTTCCACACGGGAC

a      E  T  L  R  R  T  L  G  A  L  G  I  W  S  D  Q  R  C  A  L   -
b       R  P  *  E  G  P  W  E  L  W  E  F  G  V  T  K  G  V  P  C  -
c        D  P  E  K  D  P  G  S  S  G  N  L  E  *  P  K  V  C  P  V -

       TACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGT
3901   ---------+---------+---------+---------+---------+---------+ 3960
       ATGTGTCCGCTCCTGGGACGTGGACCTACCCCCAGGGACACCCAGTTTAACCCCCCTCCA

a      Y  T  G  E  D  P  A  P  G  W  G  S  L  W  V  K  L  G  G  G   -
b       T  Q  A  R  T  L  H  L  D  G  G  P  C  G  S  N  W  G  E  V  -
c        H  R  R  G  P  C  T  W  M  G  V  P  V  G  Q  I  G  G  R  C

       GCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAAAAAAAAAAAA
3961   ---------+---------+---------+---------+---------+---------+ 4020
       CGACACCCTCATTTTATGACTTATATACTCAAAAAGTCAAAACTTTTTTTTTTTTTTTTT

a      A  V  G  V  K  Y  *  I  Y  E  F  F  S  F  E  K  K  K  K  K
b       L  W  E  *  N  T  E  Y  M  S  F  S  V  L  K  K  K  K  K  K
c        C  G  S  K  I  L  N  I  *  V  F  Q  F  *  K  K  K  K  K  K -

       AAAAAAAAA
4021   --------- 4029
       TTTTTTTTT

a      K  K  K    -
b       K  K      -
c        K  K     -
```

FIGURE 51 (cont.)

```
        TCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCA
   1681 ---------+---------+---------+---------+---------+---------+ 1740
        AGGACGTGACCGACTACTCACACATGCAGCAGCTCGACGAGTCCAGAAAGAAAATACAGT

a       S  C  T  G  *  *  V  C  T  S  S  S  C  S  G  L  S  F  M  S   -
b        P  A  L  A  D  E  C  V  R  R  R  A  A  Q  V  F  L  L  C  H  -
c         L  H  W  L  M  S  V  Y  V  V  E  L  L  R  S  F  F  Y  V  T -

        CGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGT
   1741 ---------+---------+---------+---------+---------+---------+ 1800
        GCCTCTGGTGCAAAGTTTTCTTGTCCGAGAAAAAGATGGCCTTCTCACAGACCTCGTTCA

a       R  R  P  R  F  K  R  T  G  S  F  S  T  G  R  V  S  G  A  S   -
b        G  D  H  V  S  K  E  Q  A  L  F  L  P  E  E  C  L  E  Q  V  -
c         E  T  T  F  Q  K  N  R  L  F  F  Y  R  K  S  V  W  S  K  L -

        TGCAAACCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAG
   1801 ---------+---------+---------+---------+---------+---------+ 1860
        ACGTTTGGTAACCTTAGTCTGTCGTGAACTTCTCCCACGTCGACGCCCTCGACAGCCTTC

a       C  K  P  L  E  S  D  S  T  *  R  G  C  S  C  G  S  C  R  K   -
b        A  N  H  W  N  Q  T  A  L  E  E  G  A  A  A  G  A  V  G  S  -
c         Q  T  I  G  I  R  Q  H  L  K  R  V  Q  L  R  E  L  S  E  A -

        CAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCA
   1861 ---------+---------+---------+---------+---------+---------+ 1920
        GTCTCCAGTCCGTCGTAGCCCTTCGGTCCGGGCGGGACGACTGCAGGTCTGAGGCGAAGT

a       Q  R  S  G  S  I  G  K  P  G  P  P  C  *  R  P  D  S  A  S   -
b        R  G  Q  A  A  S  G  S  Q  A  R  P  A  D  V  Q  T  P  L  H  -
c         E  V  R  Q  H  R  E  A  R  P  A  L  L  T  S  R  L  R  F  I -

        TCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAA
   1921 ---------+---------+---------+---------+---------+---------+ 1980
        AGGGGTTCGGACTGCCCGACGCCGGCTAACACTTGTACCTGATGCAGCACCCTCGGTCTT

a       S  P  S  L  T  G  C  G  R  L  *  T  W  T  T  S  W  E  P  E   -
b        P  Q  A  *  R  A  A  A  D  C  E  H  G  L  R  R  G  S  Q  N  -
c         P  K  P  D  G  L  R  P  I  V  N  M  D  Y  V  V  G  A  K  T

        CGTTCCGCAGAGAAAAGAGGCCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCG
   1981 ---------+---------+---------+---------+---------+---------+ 2040
        GCAAGGCGTCTCTTTTCTCCGGGCTCGCAGAGTGGAGCTCCCACTTCCGTGACAAGTCGC

a       R  S  A  E  K  R  G  P  S  V  S  P  R  G  *  R  H  C  S  A   -
b        V  P  Q  R  K  E  G  R  A  S  H  L  E  G  E  G  T  V  Q  R  -
c         F  R  R  E  K  R  A  E  R  L  T  S  R  V  K  A  L  F  S  V -

        TGCTCAACTACCAGCGGCCGCGGCGCCCCGGCCTCCTGGGCGCCTCTGTGTTGGGCCTGG
   2041 ---------+---------+---------+---------+---------+---------+ 2100
        ACGAGTTGATGGTCGCCGGCGCCGCGGGGCCGGAGGACCCGCGGAGACACAACCCGGACC

a       C  S  T  T  S  G  R  G  A  P  A  S  W  A  P  L  C  W  A  W   -
b        A  Q  L  R  A  G  A  A  P  R  P  P  G  R  L  C  A  G  P  G  -
c         L  N  Y  E  E  A  R  R  P  G  L  L  G  A  S  V  L  G  L  G -
```

FIGURE 51 (cont.)

```
      TGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCACACCCCCCCAAGAAGCCAC
 841  ---------+---------+---------+---------+---------+---------+ 900
      ACCTGGCTCACTGGCACCAAAGACACACCACAGTGGACGGTCTGGGGGGGTTCTTCGGTG

a      W  T  E  *  P  W  F  L  C  G  V  T  C  Q  T  R  R  R  S  H  -
b     G  P  S  D  R  G  F  C  V  V  S  P  A  R  P  A  E  E  A  T
c      D  R  V  T  V  V  S  V  W  C  H  L  P  D  P  P  K  K  P  P -

      CTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATCCGTGGGCGCGCAGCA
 901  ---------+---------+---------+---------+---------+---------+ 960
      CAGAAACCTCCCACGCGAGAGACCGTGCGCGGTGAGGGTGGGTAGGCACCCGCGCGTCGT

a      L  F  G  G  C  A  L  W  H  A  P  L  P  P  T  R  G  F  C  A
b     S  L  E  G  A  L  S  G  T  R  H  S  H  P  S  V  G  R  Q  H  -
c      L  W  R  V  R  S  L  A  R  A  T  P  T  H  P  W  A  A  S  T -

      CCACGCGGGCGCCCCATCCACATCGCGGCCACCACGTCCTGGGACACGCCTTGTCCCCCG
 961  ---------+---------+---------+---------+---------+---------+ 1020
      GGTGCGCCCGCGGGGTAGGTGTAGCGCCGGTGGTGCAGGACCCTGTGCGGAACAGGGGGC

a      P  R  G  P  P  I  H  I  A  A  T  T  S  W  D  T  P  C  P  P  .
b     H  A  G  P  P  S  T  S  R  P  P  R  P  G  T  R  L  V  P  P
c      T  R  A  F  H  P  H  R  G  H  H  V  L  G  H  A  L  S  P  G -

      GTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGNACACTGCGNCCCTC
1021  ---------+---------+---------+---------+---------+---------+ 1080
      CACATGCGGCTCTGGTTCGTGAAGGAGATGAGGAGTCCGCTGTTCNTGTGACGCNGGGAG

a      V  Y  A  E  T  K  H  F  L  Y  S  S  G  D  K  ?  T  A  ?  L  -
b     C  T  P  R  P  S  T  S  S  T  P  Q  A  T  ?  T  L  R  P  S  -
c      V  R  R  D  Q  A  L  P  L  L  L  R  R  Q  ?  H  C  ?  P  P -

      CTTCCTACTCAATATATCTGAGGCCCAGCCTGACTGGCGTTCGGGAGGTTCGTGGAGACA
1081  ---------+---------+---------+---------+---------+---------+ 1140
      GAAGGATGAGTTATATAGACTCCGGGTCGGACTGACCGCAAGCCCTCCAAGCACCTCTGT

a      L  P  T  Q  Y  I  *  G  P  A  *  L  A  F  G  R  F  V  E  T
b     F  L  L  N  I  S  E  A  Q  P  D  W  R  S  G  G  S  W  R  ?  -
c      S  Y  S  I  Y  L  R  P  S  L  T  G  V  R  E  V  R  G  D  ? -

      NTCTTTCTGGTTCCAGGCCTTGGATGCCAGGATTCCCCGCAGGTTGGCCCCGCCTGCCCCA
1141  ---------+---------+---------+---------+---------+---------+ 1200
      NAGAAAGACCAAGGTCCGGAACCTACGGTCCTAAGGGGCGTCCAACCGGGGCGGACGGGGT

a      ?  F  L  V  P  G  L  G  C  Q  D  S  P  Q  V  A  P  P  A  P  -
b     S  F  W  F  Q  A  L  D  A  R  I  P  R  R  L  P  R  L  P  Q  -
c      L  S  G  S  R  P  W  M  P  G  F  P  A  G  C  P  A  C  P  S -

      GCGNTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCC
1201  ---------+---------+---------+---------+---------+---------+ 1260
      CGCNATGACCGTTTACGCCGGGGACAAAGACCTCGACGAACCCTTGGTGCGCGTCACGGG

a      A  ?  L  A  N  A  A  P  V  S  G  A  A  W  E  P  R  A  V  P  -
b     R  Y  W  Q  M  R  F  L  F  L  E  L  L  G  N  H  A  Q  C  P  -
c      ?  T  G  K  C  G  P  C  F  W  S  C  L  G  T  T  R  S  A  P -
```

FIGURE 51 (cont.)

CTACGGGGTGTTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGG
1261 ---------+---------+---------+---------+---------+---------+ 1320
GATGCCCCACAAGGAGTTCTGCGTGACGGGCGACGCTCGACGCCAGTGGGGTCGTCGGCC

a L R G V P Q D A L P A A S C G H P S S R -
b Y G V F L K T H C P L R A A V T P A A G -
c T G C S S R R T A R C E L R S P Q Q P V -

TGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGAACACAG
1321 ---------+---------+---------+---------+---------+---------+ 1380
ACAGACACGGGCCCTCTTCGGGGTCCCGAGACACCGCCGGGGGCTCCTCCTCCTTGTGTC

a C L C P G E A P G L C G G P R G G G T Q -
b V C A R E K P Q G S V A A P E E E E H R -
c S V P G R S P R A L W R P P R R R N T D -

ACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGTGTACGGCT
1381 ---------+---------+---------+---------+---------+---------+ 1440
TGGGGGCAGCGGACCACGTCGACGAGGCGGTCGTGTCGTCGGGGACCGTCCACATGCCGA

a T P V A W C S C S A S T A A P G R C T A -
b P P S P G A A A P P A Q Q P L A G V R L -
c P R R L V Q L L R Q H S S P W Q V Y G F -

TCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCCAGGCACAACG
1441 ---------+---------+---------+---------+---------+---------+ 1500
AGCACGCCCGGACGGACGCGGCCGACCACGGGGGTCCGGAGACCCCGAGGTCCGTGTTGC

a S C G P A C A G W C P Q A S G A P G T T -
b R A G L P A P A G A P R P L G L Q A Q R -
c V R A C L R R L V P P G L W G S R H N E -

AACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCT
1501 ---------+---------+---------+---------+---------+---------+ 1560
TTGCGGCGAAGGAGTCCTTGTGGTTCTTCAAGTAGAGGGACCCCTTCGTACGGTTCGAGA

a N A A S S G T P R S S S P W G S M P S S .
b T P L P Q E H Q E V H L P G E A C Q A L .
c R R F L R N T K K F I S L G K H A K L S -

CGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCCCAGGAGCC
1561 ---------+---------+---------+---------+---------+---------+ 1620
GCGACGTCCTCGACTGCACCTTCTACTCGCACGCCCTGACGCGAACCGACGGGTCCTCGG

a R C R S * R G R * A C G T A L C C A G A -
b A A G A D V E D E R A G L R L A A Q E P
c L Q E L T W K M S V R D C A W L R R S P -

CAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTCAGGAGATCCTGGCCAAGT
1621 ---------+---------+---------+---------+---------+---------+ 1680
GTCCCCAACCGACACAAGGCCGGCGTCTCGTGGCAGACGCAGTCCTCTAGGACCGGTTCA

a Q G L A V F K P Q S T V C V R R S W P S -
b R G W L C S C R R A P S A * G D P G Q V -
c G V G C V P A A E H R L R E E I L A K -

FIGURE 50 (cont.)

2301 GCCCATGGGC ACGTCCGCAA GGCCTTCAAG AGCCACGTCT CTACCTTGAC
2351 AGACCTCCAG CCGTACATGC GACAGTTCGT GGCTCACCTG CAGGANAACA
2401 GCCCGCTGAG GGATGCCGTC GTCATCGAGC AGAGCTCCTC CCTGAATGAG
2451 GCCAGCAGTG GCCTCTTCGA CGTCTTCCTA CGCTTCATGT GCCACCACGC
2501 CGTGCGCATC AGGGGCAAGT CCTACGTCCA GTGCCAGGGG ATCCCGCAGG
2551 GCTCCATCCT CTCCACGCTG CTCTGCAGCC TGTGCTACGG CGACATGGAG
2601 AACAAGCTGT TTGCGGGGAT TCGGCGGGAC GGGCTGCTCC TGCGTTTGGT
2651 GGATGATTTC TTGTTGGTGA CACCTCACCT CACCCACGCG AAAACCTTCC
2701 TCAGGACCCT GGTCCGAGGT GTCCCTGAGT ATGGCTGCGT GGTGAACTTG
2751 CGGAAGACAG TGGTGAACTT CCCTGTAGAA GACGAGGCCC TGGGTGGCAC
2801 GGCTTTTGTT CAGATGCCGG CCCACGGCCT ATTCCCCTGG TGCGGCCTGC
2851 TGCTGGATAC CCGGACCCTG GAGGTGCAGA GCGACTACTC CAGCTATGCC
2901 CGGACCTCCA TCAGAGCCAG TCTCACCTTC AACCGCGGCT TCAAGGCTGG
2951 GAGGAACATG CGTCGCAAAC TCTTTGGGGT CTTGCGGCTG AAGTGTCACA
3001 GCCTGTTTCT GGATTTGCAG GTGAACAGCC TCCAGACGGT GTGCACCAAC
3051 ATCTACAAGA TCCTCCTGCT GCAGGCGTAC AGGTTTCACG CATGTGTGCT
3101 GCAGCTCCCA TTTCATCAGC AAGTTTGGAA GAACCCCACA TTTTTCCTGC
3151 GCGTCATCTC TGACACGGCC TCCCTCTGCT ACTCCATCCT GAAAGCCAAG
3201 AACGCAGGGA TGTCGCTGGG GGCCAAGGGC GCCGCCGGCC CTCTGCCCTC
3251 CGAGGCCGTG CAGTGGCTGT GCCACCAAGC ATTCCTGCTC AAGCTGACTC
3301 GACACCGTGT CACCTACGTG CCACTCCTGG GGTCACTCAG GACAGCCCAG
3351 ACGCAGCTGA GTCGGAAGCT CCCGGGGACG ACGCTGACTG CCCTGGAGGC
3401 CGCAGCCAAC CCGGCACTGC CCTCAGACTT CAAGACCATC CTGGACTGAT
3451 GGCCACCCGC CCACAGCCAG GCCGAGAGCA GACACCAGCA GCCCTGTCAC
3501 GCCGGGCTCT ACGTCCCAGG GAGGGAGGGG CGGCCCACAC CCAGGCCCGC
3551 ACCGCTGGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT
3601 CCGGCTGAAG GCTGAGTGTC CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA
3651 GGGCTGAGTG TCCAGCACAC CTGCCGTCTT CACTTCCCCA CAGGCTGGCG
3701 CTCGGCTCCA CCCCAGGGCC AGCTTTTCCT CACCAGGAGC CCGGCTTCCA
3751 CTCCCCACAT AGGAATAGTC CATCCCCAGA TTCGCCATTG TTCACCCCTC
3801 GCCCTGCCCT CCTTTGCCTT CCACCCCCAC CATCCAGGTG GAGACCCTGA
3851 GAAGGACCCT GGGAGCTCTG GGAATTTGGA GTGACCAAAG GTGTGCCCTG
3901 TACACAGGCG AGGACCCTGC ACCTGGATGG GGGTCCCTGT GGGTCAAATT
3951 GGGGGGAGGT GCTGTGGGAG TAAAATACTG AATATATGAG TTTTTCAGTT
4001 TTGAAAAAAA AAAAAAAAAA AAAAAAAAA

FIGURE 47 (cont.)

AGGCTGGCGTTCGGTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACT
CCCCACATAGGAATAGTCCATCCCCAGATTCGCCATTGTTCACCCTTCGCCCTGCCTTCC
TTTGCCTTCCACCCCCACCATTCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTTTGGG
AATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGG
GTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTT
TTTCAGTTTTGGAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 47 (cont.)

390
leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG

400 410
ala tyr arg phe his ala cys val leu gln leu pro phe his gln
GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG

420
gln val trp lys asn pro his phe ser cys ala ser ser leu thr
CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

430 440
arg leu pro leu leu leu his pro glu ser gln glu arg arg asp
CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

450
val ala gly gly gln gly arg arg arg pro ser ala leu arg gly
GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

460 470
arg ala val ala val pro pro ser ile pro ala gln ala asp ser
CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

480
thr pro cys his leu arg ala thr pro gly val thr gln asp ser
ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

490 500
pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys
CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

510
pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp
CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

520 530
his pro gly leu met ala thr arg pro gln pro gly arg glu gln
CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

540
thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly
ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG

550 560
arg gly gly pro his pro gly leu his arg trp glu ser glu ala
AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

564
OP
TGA GTGAGTGTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGC

CTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCGTTTTCACTTCCCCAC

FIGURE 47 (cont.)

190 200
thr tyr cys val arg arg tyr ala val val gln lys ala ala met
ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC ATG

210
gly thr ser ala arg pro ser arg ala thr ser tyr val gln cys
GGC ACG TCC GCA AGG CCT TCA AGA GCC ACG TCC TAC GTC CAG TGC

220 230
gln gly ile pro gln gly ser ile leu ser thr leu leu cys ser
CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC

240
leu cys tyr gly asp met glu asn lys leu phe ala gly ile arg
CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG ATT CGG

250 260
arg asp gly leu leu leu arg leu val asp asp phe leu leu val
CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG TTG GTG

270
thr pro his leu thr his ala lys thr phe leu arg thr leu val
ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC CTG GTC

280 290
arg gly val pro glu tyr gly cys val val asn leu arg lys thr
CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG AAG ACA

300
val val asn phe pro val glu asp glu ala leu gly gly thr ala
GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC ACG GCT

310 320
phe val gln met pro ala his gly leu phe pro trp cys gly leu
TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC GGC CTG

330
leu leu asp thr arg thr leu glu val gln ser asp tyr ser ser
CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC TCC AGC

340 350
tyr ala arg thr ser ile arg ala ser leu thr phe asn arg gly
TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC CGC GGC

360
phe lys ala gly arg asn met arg arg lys leu phe gly val leu
TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG GTC TTG

370 380
arg leu lys cys his ser leu phe leu asp leu gln val asn ser
CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC

FIGURE 46 (cont.)

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4666 gctgacccccaaagcaagcatactataggatttctagtaaagtaaaattaatctcgttattagttttgattgacttgtct 4745
4746 ttatccttatacttttaagaaagattgacagtggttgctgactactgcccacatgcccattaaacgggagtggttaaaca 4825
4826 ttaaaagtaatacatgaggctaatctcctttcatttagaataaggaaagtggttttctataatgaataatgcccgcacta 4905
4906 atgcaaaaagacgaagattatcttctaaacaaggggattaagcatatccgaaggaaaagagagtaatatacccagtgtt 4985
4986 gttgaagaaagcaaggataatttggaacaagcttctgcagatgacaggctaaattttggtgaccgaattttggtaaaagc 5065
5066 cccaggttatccatggtggccggccttgctactgagacgaaaagaaactaaggatagtttgaatactaatagctcattta 5145
5146 atgtcttatataaggttttgtttttcctgacttcaattttgcatgggtgaaaagaaatagtgttaagccattattggat 5225
5226 tccgaaatagccaaatttcttggttcctcaaagcggaagtctaaagaacttattgaagcttatgaggcttcaaaaactcc 5305
5306 tcctgatttaaaggaggaatcttccaccgatgaggaaatggatagcttatcagctgctgaggagaagcctaatttttgc 5385
5386 aaaaaagaaaatatcattgggagacatctcttgatgaatcagatgcggagagtatctccagcggatccttgatgtcaata 5465
5466 acttctatttctgaaatgtatggtcctactgtcgcttcgacttctcgtagctctacgcagttaagtgaccaaaggtacc  5544
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FIGURE 46 (cont.)

```
3533 ctaatgaaactag ATA GGA AAT TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA 3593
693                I   G   N   S   Q   Y   L   Q   K   V   G   I   P   Q   G   S  708

3594 ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA TCG 3653
709  I   L   S   S   F   L   C   H   F   Y   M   E   D   L   I   D   E   Y   L   S  728

3654 TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT TTC CTC TTT ATA ACA 3713
729  F   T   K   K   K   G   S   V   L   L   R   V   V   D   D   F   L   F   I   T  748

3714 GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT TTA TCT TTA AGA G gtgagttgctgtcattcc 3777
749  V   N   K   K   D   A   K   K   F   L   N   L   S   L   R   G                    764

3778 taagttctaaccgttgaag GA TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA 3840
765                        F   E   K   H   N   F   S   T   S   L   E   K   T   V  778

3841 ATA AAC TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC AAG AAA 3900
779  I   N   F   E   N   S   N   G   I   I   N   N   T   F   F   N   E   S   K   K  798

3901 AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TGT 3960
799  R   M   P   F   F   G   F   S   V   N   M   R   S   L   D   T   L   L   A   C  818

3961 CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG 4020
819  P   K   I   D   E   A   L   F   N   S   T   S   V   E   L   T   K   H   M   G  838

4021 AAA TCT TTT TTT TAC AAA ATT CTA AG gtatactgtgtaactgaataatagctgacaaataatcag A TCG 4089
839  K   S   F   F   Y   K   I   L   R                                            S  848

4090 AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT 4149
849  S   L   A   S   F   A   Q   V   F   I   D   I   T   H   N   S   K   F   N   S  868

4150 TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA 4209
869  C   C   N   I   Y   R   L   G   Y   S   M   C   M   R   A   Q   A   Y   L   K  888

4210 AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gtgagtacttattttaactaga 4274
889  R   M   K   D   I   F   I   P   Q   R   M   F   I   T   D                        903

4275 aaagtcattaattaaccttag AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA AAG TTG GCC 4339
904                          L   L   N   V   I   G   R   K   I   W   K   K   L   A  917

4340 GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgtc 4401
918  E   I   L   G   Y   T   S   R   R   F   L   S   S   A   E   V   K   W            935

4402 ggtctcgagacttcagcaatattgacacatcag G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA 4468
936                                       L   F   C   L   G   M   R   D   G   L   K  946

4469 CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT 4528
947  P   S   F   K   Y   H   P   C   F   E   Q   L   I   Y   Q   F   Q   S   L   T  966

4529 GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA CAT AGA AGA ATA 4588
967  D   L   I   K   P   L   R   P   V   L   R   Q   V   L   F   L   H   R   R   I  986

4589 GCT GAT TAA tgtcattttcaatttattatatacatccctttattactggtgtcttaaacaatattattactaagtata 4665
987  A   D   •                                                                        989
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FIGURE 46 (cont.)

2337 TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TTA ATG AGT AAC ATA AAG 2396

376 F L K L S R Y E S F S L H Y L M S N I K 395

2397 gtaatatgccaaatttttttaccattaattaacaatcag ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA 2465

396 I S E I E W L V L G 405

2466 AAA AGG TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG 2525

406 K R S N A K M C L S D F E K R K Q I F A 425

2526 GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCT TTT TTT TAT 2585

426 E F I Y W L Y N S F I I P I L Q S F F Y 445

2586 ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA 2645

446 I T E S S D L R N R T V Y F R K D I W K 465

2646 CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG 2705

466 L L C R P F I T S M K M E A F E K I N E 485

2706 gtattttaaagtatttttgcaaaaagctaatattttcag AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT 2775

486 N N V R M D T Q K T 495

2776 ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT ACC TTT CGT CTC ATT ACG 2835

496 T L P P A V I R L L P K K N T F R L I T 515

2836 AAT TTA AGA AAA AGA TTC TTA ATA AAG gtattaatttttggtcatcaatgtactttacttctaatctatta 2906

516 N L R K R F L I K 524

2907 ttagcag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG 2967

525 M G S N K K M L V S T N Q T L R P V 542

2968 GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG 3027

543 A S I L K H L I N E E S S G I P F N L E 562

3028 GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gtaat 3088

563 V Y M K L L T F K K D L L K H R M F G 581

3089 tatataatgcgcgattcctcattattaattttgcag G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA 3155

582 R K K Y F V R I D I 591

3156 AAA TCC TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG AAA CTC 3215

592 K S C Y D R I K Q D L M F R I V K K K L 611

3216 AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT GCA ACA AGT GAC CGA GCT 3275

612 K D P E F V I R K Y A T I H A T S D R A 631

3276 ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC TAT T gtaagtttatttttcattggaatttttaacaa 3343

632 T K N F V S E A F S Y F 643

3344 atttttttag TT GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA 3405

644 D M V P F E K V V Q L L S M K T 659

3406 TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT TCT GAA ATT TTT 3465

660 S D T L F V D F V D Y W T K S S S E I F 679

3466 AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT AAG gtataccaattgttgaattgtaataaca 3532

680 K M L K E H L S G H I V K 692

FIGURE 46 (cont.)

1199 AAA TGC TCA CAG TCA GAG gtatatatattttgttttgatttttttctattcgggatagctaatatatgggcag 1272
81 K C S Q S E 86

1273 CTA ATA GCG AAT GTT GTA AAA CAG ATG TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA 1332
87 L I A N V V K Q M F D E S F E R R R N L 106

1333 CTG ATG AAA GGG TTT TCC ATG gtaaggtattctaattgtgaaatatttacctgcaattactgtttcaaagaga 1405
107 L M K G F S M 113

1406 ttgtatttaaccgataaag AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA AAC GGA GTA CAA AAT 1469
114 N H E D F R A M H V N G V Q N 128

1470 GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA 1529
129 D L V S T F P N Y L I S I L E S K N W Q 148

1530 CTT TTG TTA GAA AT gtaaataccggttaagatgttgcgcactttgaacaagactgacaagtatag T ATC GGC 1601
149 L L L E I I G 155

1602 AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC 1661
156 S D A M H Y L L S K G S I F E A L P N D 175

1662 AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG 1721
176 N Y L Q I S G I P L F K N N V F E E T V 195

1722 TCA AAA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA 1781
196 S K K R K R T I E T S I T Q N K S A R K 215

1782 GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT 1841
216 E V S W N S I S I S R F S I F Y R S S Y 235

1842 AAG AAG TTT AAG CAA G gtaactaatactgttatccttcataactaatttag AT CTA TAT TTT AAC
1907
236 K K F K Q D L Y F N 245

1908 TTA CAC TCT ATT TGT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG 1967
246 L H S I C D R N T V H M W L Q W I F P R 265

1968 CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA 2027
266 Q F G L I N A F Q V K Q L H K V I P L V 285

2028 TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA 2087
286 S Q S T V V P K R L L K V Y P L I E Q T 305

2088 GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT 2147
306 A K R L H R I S L S K V Y N H Y C P Y I 325

2148 GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG 2207
326 D T H D D E K I L S Y S L K P N Q V F A 345

2208 TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA 2267
346 F L R S I L V R V F P K L I W G N Q R I 365

2268 TTT GAG ATA ATA TTA AAA G gtattgtataaaatttattaccactaacgattttaccag AC CTC GAA ACT 2336
366 F E I I L K D L E T 375

B

Figure 42

```
Sp_Tlp1p    1  ----------MTEHHT[illegible]ILRFLENQYVVYLCT  24
Sc_Est2p    1  --------------------------MKILFEF  7
Ea_p123     1  MEVDVDNQADNHGIHSALKTCEEIKEAKTLYSW  33

Sp_Tlp1p   25  LNDYVQLVLRGSPA[illegible]S[illegible]SNICERLRSDVQTSFS  57
Sc_Est2p    8  IQDKLDIDLQTN--[illegible]T[illegible]K---ENLKCGHFNGLD  35
Ea_p123    34  IQKVIRCRNQSQ--[illegible]H[illegible]K---DLEDIKIFAQTN  61

Sp_Tlp1p   58  IFLHSTVVGFDSKPDEQVQFSSPKCSQSEL[illegible]AN  90
Sc_Est2p   36  EILTTCFALPNSR-KIALPCLPGDLSHKAV[illegible]DH  67
Ea_p123    62  IVATPRDYNEEDFKVIARKEVFSTGLMIEL[illegible]DK  94

Sp_Tlp1p   91  VVKQMFDESFERRR-NLLMK[illegible]FSMNHEDFRAMH  122
Sc_Est2p   68  CIIYLLTQELYN---NVLTFGYKIARNED----  93
Ea_p123    95  CLVELLSSSDVSDRQKLQCFGFQLKGNQ-----  122

Sp_Tlp1p  123  VNGVQNDLVSTFPNYLISILESKNWQLLLEIIG  155
Sc_Est2p   94  ---VNNSLFCHSANVNVTLLKGAAWKMFHSLVG  123
Ea_p123   123  ---LAKTHLLTALSTQKQYFFQDEWNQVRAMIG  152

Sp_Tlp1p  156  SDAMHY[illegible]LSKGSIFEALPNDNYL[illegible]IS[illegible]IPLFKN  188
Sc_Est2p  124  TYAFVD[illegible]LINYTVIQFN-GQFFT[illegible]IV[illegible]NRCNEP  155
Ea_p123   153  NELFRH[illegible]YTKYLIFQRTSEQTLV[illegible]FC[illegible]NNVFDH  185

Sp_Tlp1p  189  NVFEETVSKKRKRTIETSITQN---KSARKE[illegible]S  218
Sc_Est2p  156  HLPPKWVQ--RSSSSSATAAQI---KQLTEP[illegible]T  183
Ea_p123   186  LKVNDKFDK-KQKGGAADMNEPRCCSTCKYN[illegible]K  217

Sp_Tlp1p  219  WNSISISRFSIFYRSSYKKFKQDLYFNLHSICD  251
Sc_Est2p  184  N----------------KQFLHKLNINSSSFFP  200
Ea_p123   218  NEK--DHFLNNINVPNWNNMKSRTRIFYCTHFN  248

Sp_Tlp1p  252  RNTVHMWLQWIFPRQFGLINAFQVKQLHKVIPL  284
Sc_Est2p  201  --------YSKILPSSS---SIKKLTDLREAIFP  223
Ea_p123   249  R-------NNQFFKKHEFVSNKNNISAMDRAQTI  275

Sp_Tlp1p  285  VS----QSTVVPKRLLKVYPLIEQTAKRLHRIS  313
Sc_Est2p  224  TN----LVKIPQRLKVRINLTLQKLLKRHKRLN  252
Ea_p123   276  FTNIFRFNRIRKKLKDKVIEKIAYMLEKVKDFN  308

Sp_Tlp1p  314  LSKVYNHY[illegible]YID-THDDEKILSYSLKPNQ---  342
Sc_Est2p  253  YVSILNSI[illegible]PLEGTVLDLSHLSRQSPKER---  282
Ea_p123   309  FNYYLTKS[illegible]LPENWRERKQKIENLINKTREEK  341

Sp_Tlp1p  343  -----------------[illegible]FA[illegible]LRSILVRVF[illegible]KLI  359
Sc_Est2p  283  -----------------[illegible]LK[illegible]IIVILQKLL[illegible]QEM  299
Ea_p123   342  SKYYEELFSYTTDNKC[illegible]TQ[illegible]INEFFYNIL[illegible]KDF  374

Sp_Tlp1p  360  WGNQRIFEIIL[illegible]DLETFLK[illegible]SRYESFSLHY[illegible]MS  392
Sc_Est2p  300  FGSKKNKGKII[illegible]NLNLLLS[illegible]PLNGYLPFDS[illegible]LK  332
Ea_p123   375  LTG-RNRKNFQ[illegible]KVKKYVE[illegible]NKHELIHKNL[illegible]LE  406

Sp_Tlp1p  393  NIKISEIE[illegible]LVLGKRSNAKMCLSDF[illegible]KRKQIFA  425
Sc_Est2p  333  KLRLKDFRWLFIS---DIWFTKHNF[illegible]NLNQLAI  362
Ea_p123   407  KINTREISWMQVETS-AKHFYYFDH[illegible]N-IYVLW  437

Sp_Tlp1p  426  EFIY[illegible]LYNSFIIPILQS[illegible]I[illegible]SSDLRNRTV[illegible]  458
Sc_Est2p  363  CFIS[illegible]LFRQLIPKIIQT[illegible]C[illegible]ISSTVT-IV[illegible]  394
Ea_p123   438  KLLR[illegible]IFEDLVVSLIRC[illegible]V[illegible]QQKSYSKTY[illegible]  470

Sp_Tlp1p  459  F[illegible]KDI[illegible]KLLCRPF[illegible]TSMKMEAFEKINENNVRMD  491
Sc_Est2p  395  F[illegible]HDT[illegible]NKLITPF[illegible]VEYFKTYLVENNVCRNHNS  427
Ea_p123   471  Y[illegible]KNI[illegible]DVIMKMS[illegible]ADLKKETLAEVQEKEVEEW  503

Sp_Tlp1p  492  TQKTTLPPAVI[illegible]LL[illegible]--NT[illegible]L[illegible]TNLRKRFL  522
Sc_Est2p  428  YTLSNFNHSKM[illegible]II[illegible]SNNE[illegible]I[illegible]AIPCRGAD  460
Ea_p123   504  KKSLGFAPQKL[illegible]LI[illegible]--TT[illegible]P[illegible]MTFNKKIV  534

Sp_Tlp1p  523  IKMGSNKKMLVSTNQTLRPVASI[illegible]KH[illegible]I[illegible]E---  552
Sc_Est2p  461  EEE--FTIYKENHKNAIQPTQKI[illegible]EY[illegible]R[illegible]KRPT  491
Ea_p123   535  NSD--RKTTKLTTNTKLLNSHLM[illegible]KT[illegible]K[illegible]R-MF  564

Sp_Tlp1p  553  ESSGIPFNLEVYMKLLTFKKDLL[illegible]HRMFGR-KK  584
Sc_Est2p  492  SFTKIYSPTQIADRIKEFKQRLL[illegible]KFNNVLPEL  524
Ea_p123   565  KDPFGFAVFNYDDVMKKYEEFVC[illegible]WKQVGQPKL  597

Sp_Tlp1p  585  Y[illegible]VRI[illegible]IKS[illegible]RIKQDLMFRIV[illegible]KKLKDPE-[illegible]  616
Sc_Est2p  525  Y[illegible]MKF[illegible]VKS[illegible]SIPRMECMRIL[illegible]DALKNENG[illegible]  557
Ea_p123   598  F[illegible]ATM[illegible]IEK[illegible]SVNREKLSTFL[illegible]TTKLLSSD[illegible]  630

Sp_Tlp1p  617  VIRKYATIHATSDRATKN----------------  634
Sc_Est2p  558  FVRSQYFFNTNTQ---------------------  570
Ea_p123   631  WIMTAQILKRKNNIVIDSKNFRKKEMKDYFRQK  663

Sp_Tlp1p  635  FVSEAFSYFDMVPFEK[illegible]VQLLS--MKTSDT[illegible]FV  665
Sc_Est2p  571  -----------VLKLFN[illegible]VNASR--VPKPYE[illegible]YI  591
Ea_p123   664  FQKIALEGGQYPTLFS[illegible]LENEQNDLNAKKT[illegible]IV  696

Sp_Tlp1p  666  DFVDYWTKSSSEIFKMLKEHLSGHIVKIQNSQ[illegible]  698
Sc_Est2p  592  DNVRTVHLSNQDVINVVEMEIFKTALWVEDKC[illegible]  624
Ea_p123   697  EAKQRNYFKKDNLLQPVINICQYNYINFNQKF[illegible]  729

Sp_Tlp1p  699  LQKV[illegible]IP[illegible]SIL[illegible]SFLCHFYMED[illegible]IDEYLS[illegible]TK  731
Sc_Est2p  625  IRED[illegible]LF[illegible]SSL[illegible]APIVDLVYDD[illegible]LEFYSE[illegible]KA  657
Ea_p123   730  KQTK[illegible]IP[illegible]LCV[illegible]SILSSFYYAT[illegible]EESSLG[illegible]LR  762

Sp_Tlp1p  732  KKG--------SVLLRVV[illegible]F[illegible]F[illegible]TVNKKDAKK  756
Sc_Est2p  658  SPSQD------TLILKLA[illegible]F[illegible]I[illegible]STDQQQVIN  684
Ea_p123   763  DESMNPENPNVNLLMRLT[illegible]Y[illegible]L[illegible]TTQENNAVL  795

Sp_Tlp1p  757  FLNLSLRGFEKHNFSTSLE[illegible]TVINFEN[illegible]NG---  786
Sc_Est2p  685  IKKLAMGGFQKYNAKANRD[illegible]ILAVSSQ[illegible]D----  713
Ea_p123   796  FIEKLINVSRENQFKFNMK[illegible]LQTSFPL[illegible]PSKFA  828

Sp_Tlp1p  787  ---IINNTFFNESKKRMPFFGFSVNMRSLDTLL  816
Sc_Est2p  714  ----DDTVIQFCA---MHIFVKELEVWKHSSTM  739
Ea_p123   829  KYQMDSVEEQNIVQDYCDWIGISIDMKTLALMP  861

Sp_Tlp1p  817  ACPKIDEALFNSTSVELTKHMQKSFFY[illegible]ILRSS  849
Sc_Est2p  740  NNFHIRSKSSKGIFRSLIALFNTRISY[illegible]TIDTN  772
Ea_p123   862  NINLRIEGILCTLNLNMQTKKASMWLK[illegible]KLKSF  894

Sp_Tlp1p  850  [illegible]ASFAQVFIDITHNSKFNSCCNIYRLGYSMCMR  882
Sc_Est2p  773  [illegible]NSTNTVLMQIDHVVKNISEC------------  793
Ea_p123   895  [illegible]MNNITHYFRKTITTEDFANKTLNKLFISGGYK  927

Sp_Tlp1p  883  AQAYLKRM[illegible]IFIPQRMFITDLLNVIGRK[illegible]WKK  915
Sc_Est2p  794  ---YKSAF[illegible]LSIN--VTQNMQFHSFLQR[illegible]IEM  821
Ea_p123   928  YMQCAKEY[illegible]HFKKNLAMSSMIDLEVSKI[illegible]YSV  960

Sp_Tlp1p  916  LAEILGYTSRRFLSSAEVKWLFCLGMRDG[illegible]KPS  948
Sc_Est2p  822  TVSGCPITKCDPLIEYEVRFTILNGFLES[illegible]SSN  854
Ea_p123   961  TRAFFKYLVCNIKDTIFGEEHYPDFFLST[illegible]KHF  993

Sp_Tlp1p  949  FKYHPCFEQLIYQ[illegible]QSLTDLIKPLRPV[illegible]RQVLF  981
Sc_Est2p  855  TS-----------K[illegible]KDNIILLRKEIQH[illegible]QAYIY  877
Ea_p123   994  IEIFS---TKKYI[illegible]NRVCMILKAKEAK[illegible]KSDQC  1023

Sp_Tlp1p  982  LHRRIAD-  988
Sc_Est2p  878  IYIHIVN-  884
Ea_p123  1024  QSLIQYDA  1031
```

Fig. 42

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FIGURE 30 (cont.)

ATGgtacgtgtcggtctcgagacttcagcaatattgacacatcagGCTTTTTTGTCTTGGAATGAGAGATGGTTTGAAACCCTCTT
TCAAATATCATCCATGCTTCGAACAGCTAATATACCAATTTCAGTCATTGACTGATCTTATCAAGCCGC
TAAGACCAGTTTTGCGACAGGTGTTATTTTTACATAGAAGAATAGCTGATTAAtgtcatttcaattattatatacatcctt
tattactggtgtcttaaacaatattattactaagtatagctgacccccaaagcaagcatactataggatttctagtaaagtaaaattaatctcgttattagttttgattgacttgtcttt
atccttatactttaagaaagattgacagtggttgctgactactgcccacatgcccattaaacgggagtggttaaacattaaaagtaatacatgaggctaatctcctttcatttag
aataaggaaagtggttttctataatgaataatgcccgcactaatgcaaaaagacgaagattatcttctaaacaaggggattaagcatatccgaaggaaaagagagtaatat
acccagtgttgttgaagaaagcaaggataatttggaacaagcttctgcagatgacaggctaaattttggtgaccgaattttggtaaaagccccaggttatccatggtggccg
gccttgctactgagacgaaaagaaactaaggatagtttgaatactaatagctcatttaatgtcttatataaggttttgtttttcctgacttcaattttgcatgggtgaaaagaaata
gtgttaagccattattggattccgaaatagccaaatttcttggttcctcaaagcggaagtctaaagaacttattgaagcttatgaggcttcaaaaactcctcctgatttaaaggag
gaatcttccaccgatgaggaaatggatagcttatcagctgctgaggagaagcctaattttttgcaaaaaagaaaatatcattgggagacatctcttgatgaatcagatgcgga
gagtatctccagcggatccttgatgtcaataacttctatttctgaaatgtatggtcctactgtcgcttcgacttctcgtagctctacgcagttaagtgaccaaggtacc

FIGURE 12 (cont.)

```
       TTAAAGATTTCAAAAATTCCAGGTAAGAGAGATACATTCATTAAAATTCATATATTATAG
1081   ------------------------------------------------------------ 1140
       AATTTCTAAAGTTTTTAAGGTCCATTCTCTCTATGTAAGTAATTTTAAGTATATAATATC

a      L  K  I  S  K  I  P  G  K  R  D  T  F  I  K  I  H  I  L  ·  -
b       ·  R  F  Q  K  F  Q  V  R  E  I  H  S  L  K  F  I  Y  Y  S -
c        K  D  F  K  N  S  R  ·  E  R  Y  I  H  ·  N  S  Y  I  I  V-

       TTTTTCATTTCACAGCTGTTATTTTCTTTTATCTTAACAATATTTTTTGATTAGCTCGAA
1141   ------------------------------------------------------------ 1200
       AAAAAGTAAAGTGTCGACAATAAAAGAAAATAGAATTGTTATAAAAAACTAATCGACCTT

a      F  F  I  S  Q  L  L  F  S  F  I  L  T  I  F  F  D  ·  L  E  -
b       F  S  F  H  S  C  Y  F  L  L  S  ·  Q  Y  F  L  I  S  W  K -
c        F  H  F  T  A  V  I  F  F  Y  L  N  N  I  F  C  L  A  C  S-

       GTAAAAAGTATCAAATAAGAGAAGCGCTAGACTGAGGTAACTTAGCTTATTCACATTCAT
1201   ------------------------------------------------------------ 1260
       CATTTTTCATAGTTTATTCTCTTCGCGATCTGACTCCATTGAATCGAATAAGTGTAAGTA

a      V  K  S  I  K  ·  E  K  R  ·  T  E  V  T  ·  L  I  H  I  H  -
b       ·  K  V  S  N  K  R  S  A  R  L  R  ·  L  S  L  F  T  F  I -
c        K  K  Y  Q  I  R  E  A  L  D  C  G  N  L  A  Y  S  H  S  ·-

       AGATCGACCTTCATATATCCAATACGATGATAAGGAAACAGCAGTCATCCGTTTTAAAAA
1261   ------------------------------------------------------------ 1320
       TCTAGCTGGAAGTATATAGGTTATGCTACTATTCCTTTGTCGTCAGTAGGCAAAATTTTT

a      R  S  T  F  I  Y  P  I  R  C  ·  G  N  S  S  H  P  F  ·  K  -
b       D  R  P  S  Y  I  Q  Y  D  D  K  E  T  A  V  I  R  F  K  N -
c        I  D  L  H  I  S  N  T  H  I  R  K  Q  Q  S  S  V  L  K  I-

       TAGTGCTATGAGGACTAAATTTTTAGAGTCAAGAAATGGAGCCGAAATCTTAATCAAAAA
1321   ------------------------------------------------------------ 1380
       ATCACGATACTCCTGATTTAAAAATCTCAGTTCTTTACCTCGGCTTTAGAATTAGTTTTT

a      ·  C  Y  E  D  ·  I  F  R  V  K  K  W  S  R  N  L  N  Q  K  -
b       S  A  H  R  T  K  F  L  E  S  R  N  G  A  E  I  L  I  K  K -
c        V  L  C  G  L  N  F  ·  S  Q  E  H  E  P  K  S  ·  S  K  R-

       GAATTGCCGTCGATATTGCAAAAGAATCGAACTCTAAATCTTTCGTTAATAAGTATTACCA
1381   ------------------------------------------------------------ 1440
       CTTAACGCAGCTATAACGTTTTCTTAGCTTGAGATTTAGAAAGCAATTATTCATAATGGT

a      E  L  R  R  Y  C  K  R  I  E  L  ·  I  F  R  ·  ·  V  L  P  .
b       N  C  V  D  I  A  K  E  S  N  S  K  S  F  V  N  K  Y  Y  Q .
c        I  A  S  I  L  Q  K  N  R  T  L  N  L  S  L  I  S  I  T  N.

       ATCTTGATTGATTGAAGAGATTGACGAGGCAACTCCACAGAAGATCATTAAAGAAATAAA
1441   ------------------------------------------------------------ 1500
       TAGAACTAACTAACTTCTCTAACTGCTCCGTTGACGTGTCTTCTAGTAATTTCTTTATTT

a      I  L  I  D  C  R  D  ·  R  G  N  C  T  E  D  H  ·  R  N  K  .
b       S  C  L  I  E  E  I  D  E  A  T  A  Q  K  I  I  K  E  I  K .
c        L  D  C  L  K  R  L  T  R  Q  L  H  R  R  S  L  K  K  ·  S.

       GTAACTTTTATTAATTAGAGAATAAACTAAATTACTAATATAGAGATCAGCGATCTTCAA
1501   ------------------------------------------------------------ 1560
       CATTGAAAATAATTAATCTCTTATTTGATTTAATGATTATATCTCTAGTCGCTAGAAGTT

a      V  T  F  I  N  ·  R  I  N  ·  I  T  N  I  E  I  S  D  L  Q  .
b       ·  L  L  L  I  R  E  ·  T  K  L  L  I  ·  R  S  A  I  F  N .
c        N  F  Y  ·  L  E  N  K  L  N  Y  ·  Y  R  D  Q  R  S  S  I-

       TTGACGAAATAAAAGCTGAACTAAAGTTAGACAATAAAAAATACAAACCTTGGTCAAAAT
1561   ------------------------------------------------------------ 1620
       AACTGCTTTATTTTCGACTTGATTTCAATCTGTTATTTTTTATGTTTGGAACCAGTTTTA

a      L  T  K  ·  K  L  N  ·  S  ·  T  I  K  N  T  N  L  G  Q  N  .
b       C  R  N  K  S  C  T  K  V  R  Q  ·  K  I  Q  T  L  V  K  I .
c        D  E  I  K  A  E  L  K  L  D  N  K  K  Y  K  P  W  S  K  Y.

       ATTGAGGAAGGAAAAGAAGACCACTTAGCAAAAGAAAAAATAAGGCAATAAATAAAATGA
1621   ------------------------------------------------------------ 1680
       TAACTCCTTCCTTTTCTTCTGGTCAATCGTTTTCTTTTTTATTCCGTTATTTATTTTACT

a      I  E  E  G  K  E  D  Q  L  A  K  E  K  I  R  Q  ·  I  K  C  .
b       L  R  K  E  K  K  T  S  ·  Q  K  K  K  ·  G  N  K  ·  N  E .
c        C  G  R  K  R  R  P  V  S  K  R  K  N  K  A  I  N  K  H  S-
```

FIGURE 12 (cont.)

```
        GTACAGAAGTGAAGAAATAAAAGATTTATTTTTTTCAATAATTTATTGAAAAGAGCCCTT
   1681 ------------------------------------------------------------ 1740
        CATGTCTTCACTTCTTTATTTTCTAAATAAAAAAAGTTATTAAATAACTTTTCTCCCCAA

a        V  Q  K  C  R  N  K  R  F  I  F  F  N  N  L  L  K  R  G  V   .
b         Y  R  S  E  E  I  K  D  L  F  F  S  I  I  Y  C  K  E  G  F  .
c          T  E  V  K  K  *  K  I  Y  F  F  Q  *  F  I  E  K  R  G  F .

        TTCGCCTTTTCGGGTTTTGGGG
   1741 ---------------------- 1762
        AACCCCAAAACCCCAAAACCCC

a        L  G  F  W  G  F  G    .
b         W  G  F  G  V  L  G   .
c          G  V  L  G  F  W     .
```

FIGURE 12 (cont.)

```
481  CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAGACAAACTCGCTAT
     ------------------------------------------------------------  540
     GTATACTCTTACTCAGTTTCCTAGAGCTATGTAGTCTGAATGGTTTCTGTTTGAGCGATA

a     H  M  R  M  S  Q  R  I  S  I  H  Q  T  Y  Q  R  Q  T  R  Y  -
b     I  C  E  C  V  K  G  S  R  Y  I  R  L  T  K  D  K  L  A  I  -
c     Y  E  N  E  S  K  D  L  D  T  S  D  L  P  K  T  N  S  L  •  -

541  AAAACCCAAGAAAAAGTTTGATAATCGAACAGCAGAAGAACTTATTGCATTTACTATTCG
     ------------------------------------------------------------  600
     TTTTGCGTTCTTTTTCAAACTATTAGCTTGTCGTCTTCTTGAATAACGTAAATGATAAGC

a     K  T  Q  E  K  V  C  •  S  N  S  R  R  T  Y  C  I  Y  Y  S  -
b     K  R  K  K  K  F  D  N  R  T  A  E  E  L  I  A  F  T  I  R  -
c     N  A  R  K  S  L  I  I  E  Q  Q  K  N  L  L  H  L  L  F  V  -

601  TATGGGTTTTATTACAATTGTTTTAGGTATCGACGGTGAACTCCCGAGTCTTGAGACAAT
     ------------------------------------------------------------  660
     ATACCCAAAATAATGTTAACAAAATCCATAGCTGCCACTTGAGGGCTCAGAACTCTGTTA

a     Y  G  F  Y  Y  N  C  F  R  Y  R  R  C  T  P  E  S  C  D  N  -
b     M  G  F  I  T  I  V  L  G  I  D  G  E  L  P  S  L  E  T  I  -
c     W  V  L  L  Q  L  F  •  V  S  T  V  N  S  R  V  L  R  Q  L  -

661  TGAAAAAGCTGTTTACAACTGAAGGAATCGCAGTTCTGAAAGTTCTGATGTGTATGCCAT
     ------------------------------------------------------------  720
     ACTTTTTCGACAAATGTTGACTTCCTTAGCGTCAAGACTTTCAAGACTACACATACGGTA

a     C  K  S  C  L  Q  L  K  E  S  Q  F  C  K  F  •  C  V  C  H  -
b     E  K  A  V  Y  N  C  R  N  R  S  S  E  S  S  D  V  Y  A  I  -
c     K  K  L  F  T  T  E  G  I  A  V  L  K  V  L  M  C  M  P  L  -

721  TATTTTGTGAATTAATCTCAAATATCTTATCTCAATTTAATGGATAGCTATAGAAACAAA
     ------------------------------------------------------------  780
     ATAAAACACTTAATTAGAGTTTATAGAATAGAGTTAAATTACCTATCGATATCTTTGTTT

a     Y  F  V  N  •  S  Q  I  S  Y  L  N  L  M  D  S  Y  R  N  K  -
b     I  L  C  I  N  L  K  Y  L  I  S  I  •  W  I  A  I  E  T  N  -
c     F  C  E  L  I  S  N  I  L  S  Q  F  N  G  •  L  •  K  Q  T  -

781  CCAAATAAACCATGCAAGTTTAATGGAATATACGTTAAATCCTTTGGGACAAATGCACAC
     ------------------------------------------------------------  840
     GGTTTATTTGGTACGTTCAAATTACCTTATATGCAATTTAGGAAACCCTGTTTACGTGTG

a     P  N  K  P  C  K  F  N  G  I  Y  V  K  S  F  G  T  N  A  H  -
b     Q  I  N  H  A  S  L  M  E  Y  T  L  N  P  L  G  Q  M  H  T  -
c     K  •  T  M  Q  V  •  W  N  I  R  •  I  L  W  D  K  C  T  L  -

841  TGAATTTATATTGCATTCTTAAAGCATAGATACACAGAATGCTTTAGAGACTGATTTAGC
     ------------------------------------------------------------  900
     ACTTAAATATAACGTAAGAATTTCGTATCTATGTGTCTTACGAAATCTCTGACTAAATCG

a     C  I  Y  I  C  F  L  K  H  R  Y  T  E  C  F  R  D  C  F  S  -
b     E  F  I  L  D  S  •  S  I  D  T  Q  N  A  L  E  T  D  L  A  -
c     N  L  Y  W  I  L  K  A  •  I  H  R  M  L  •  R  L  I  •  L  -

901  TTACAACAGATTACCTGTTTTGATTACTCTTGCTCATCTCTTATATCTTTAAAAGAAGCA
     ------------------------------------------------------------  960
     AATGTTGTCTAATGGACAAAACTAATGAGAACGAGTAGAGAATATAGAAATTTTCTTCGT

a     L  Q  Q  I  T  C  F  D  Y  S  C  S  S  L  I  S  L  K  E  A  -
b     Y  N  R  L  P  V  L  I  T  L  A  H  L  L  Y  L  •  K  K  Q  -
c     T  T  D  Y  L  F  C  L  L  L  L  I  S  Y  I  F  K  R  S  R  -

961  GGCGAAATGAAAAGAAGACTAAAGAAAGAGATTTCAAAATTTGTTGATTCTTCTGTAACC
     ------------------------------------------------------------  1020
     CCGCTTTACTTTTCTTCTGATTTCTTTCTCTAAAGTTTTAAACAACTAAGAAGACATTGG

a     G  E  M  K  R  R  L  K  K  E  I  S  K  F  V  D  S  S  V  T  -
b     A  K  C  K  E  D  •  R  K  R  F  Q  N  L  L  I  L  L  •  P  -
c     R  N  E  K  K  T  K  E  R  D  F  K  I  C  C  F  F  C  N  R  -

1021 CGAATTAACAACAAGAATATTAGCAACGAAAAAGAAGAAGAGCTATCACAATCCTGATTC
     ------------------------------------------------------------  1080
     GCTTAATTGTTGTTCTTATAATCGTTGCTTTTTCTTCTTCTCGATAGTGTTAGGACTAAG

a     G  I  N  N  K  N  I  S  N  E  K  E  E  E  L  S  Q  S  C  F  -
b     E  L  T  T  R  I  L  A  T  K  K  K  K  S  Y  H  N  P  D  S  -
c     N  •  Q  Q  E  Y  •  Q  R  K  R  R  R  A  I  T  I  L  I  L  -
```

FIGURE 9 (cont.)

2351 GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA
2401 CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC
2451 TTTTGATTAC AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT
2501 ATAAACGTAA GTCGTGAAAA TGGATTTAAA TTCAATATGA AGAAACTACA
2551 GACTAGTTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA
2601 GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC
2651 TCAATTGATA TGAAAACTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT
2701 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT
2751 CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC
2801 CATTATTTTA GAAAGACGAT TACAACCGAA GACTTTGCGA ATAAAACTCT
2851 CAACAAGTTA TTTATATCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG
2901 AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG TATGATCGAC
2951 TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA
3001 CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG
3051 ACTTTTTCCT TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA
3101 AAGTACATTT TCAACAGAGT TTGCATGATC CTCAAGGCAA AAGAAGCAAA
3151 GCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA
3201 CTATTCTAAC TTATTTTGGA AAGTTAATTT TCAATTTTTG TCTTATATAC
3251 TGGGGTTTTG GGGTTTTGGG GTTTTGGGG

mTRT.ad -hTRT DNA align Formatte nment

```
hTCP1.2.gw       AGAGCACCGT CTGCGTGAGG AGATCCTGGC CAAGTTCCTG CACTGGCTGA   1700
mTRT.1.adj.gw    ---------- ---------- ---------- ---------- ----------
Consensus        AGAGCACCGT CTGCGTGAGG AGATCCTGGC CAAGTTCCTG CACTGGCTGA   1700

hTCP1.2.gw       TGAGTGTGTA CGTCGTCGAG CTGCTCAGGT CTTTCTTTTA TGTCACGGAG   1750
mTRT.1.adj.gw    ---------- ---------- ---------- ---------- ----------
Consensus        TGAGTGTGTA CGTCGTCGAG CTGCTCAGGT CTTTCTTTTA TGTCACGGAG   1750

hTCP1.2.gw       ACCACGTTTC AAAAGAACAG GCTCTTTTTC TACCGGAAGA GTGTCTGGAG   1800
mTRT.1.adj.gw    ---------- ---------- ---------- ---------- ----------
Consensus        ACCACGTTTC AAAAGAACAG GCTCTTTTTC TACCGGAAGA GTGTCTGGAG   1800

hTCP1.2.gw       CAAGTTGCAA AGCATTGGAA TCAGACAGCA CTTGAAGAGG GTGCAGCTGC   1850
mTRT.1.adj.gw    ---------- ---------- ---------- ---------- ----------
Consensus        CAAGTTGCAA AGCATTGGAA TCAGACAGCA CTTGAAGAGG GTGCAGCTGC   1850

hTCP1.2.gw       GGGAGCTGTC GGAAGCAGAG GTCAGGCAGC ATCGGGAAGG CAGGG---GC   1897
mTRT.1.adj.gw    ---------- ---------- --GAGGCAGC ATCNACAGAC ACTGCTAGGA     28
Consensus        GGGAGCTGTC GGAAGCAGAG GTSAGGCAGC ATGNRSARRC MMKGCTAGGM   1900

hTCP1.2.gw       GCGCTGCCTA CGTCAGACTT CGGCTTCATG GGCAAGGCTG ACGGGCTGGG   1947
mTRT.1.adj.gw    GCGCTGCCTA TCTCAGACTT CGGCTTCATG GCGAAGGCCA ACTG---GCG     75
Consensus        GCGCTGCCYA YSTCAGACTT CGGCTTCATG GCGAAGGCYR ACKGGCTGGG   1950

hTCP1.2.gw       GCGCATTGTG AACATGGACT ACGTCGTGGG AGCCAGAACG TTCCGTAGAG   1997
mTRT.1.adj.gw    GCGCATTGTG AAGATGAGTT ATAGCATGCC TGCCAGAGCT TTGGGGAGAA    125
Consensus        GCGCATTGTG AACATGRRYT AYRGCRTGGG WGCCAGARCK TTSSGCAGAR   2000

hTCP1.2.gw       AAAAGAGCGG -- ---------- GCCGAGCGTC TGACCTCGAG GGTGAAGGCA   2035
mTRT.1.adj.gw    GCAAGCAGGC CCAGCATTTC AGCGAGCGTC TGCA------- -----AGGCT    163
Consensus        RRAAGMRCGC CCAGCATTTC RCCGAGCGTC TGACCTCGAG GGTGAAGGCW   2050

hTCP1.2.gw       CTGTTCAGCG TGCTCAACTA CGAGCGGGCG CGGCGCCCGG GCCTCCTGGG   2085
mTRT.1.adj.gw    CTCTTCAGCA TGCTCAACTA TGAGCGGG-- ----AATTCG ATATCAAG--    205
Consensus        CTSTTCAGCR TGCTCAACTA YGAGCGGGCG CGGCRMYYCG RYMTCMWGGG   2100

hTCP1.2.gw       CGCCTCTTTC CTGGGCCTGG ACGATATCCA CAGGGCCTGG CGCACCTTCG   2135
mTRT.1.adj.gw    ---CT-TT-- ---------- -CGATA-CC- ---------- ----------    217
Consensus        CGCCTCTTTC CTGGGCCTGG ACGATATCCA CAGGGCCTGG CGCACCTTCG   2150

hTCP1.2.gw       TGCTGCGTGT GCGGGCCGAG GACCCGCCGC CTGGGTGTA CTTTGTCAAG   2185
mTRT.1.adj.gw    ---------- ----GCTCAG AGCAGCCGCA GCGCG----- ----------    239
Consensus        TGCTGCGTGT GCGGGCMCAG RRCMGCCGCM SKGCGTGTA CTTTGTCAAG   2200
```

FIG. 56 (2/2)

Telomerase RT Motifs (Fingers)

Motif		MOTIF 1		MOTIF 2		MOTIF A		MOTIF B'
TRT con		R iPKk		fR I		p lyF D cYD I		Y q GipQGs lS L y
hTRT	11	SRLRFIPKPDG	0	LRPIV	69	PELYFVKVDVTGAYDTI	104	YVQCQGIPQGSILSTLLCSLCY
spTRT	10	AVIRLLPKKNT	0	FRLIT	66	RKKYFVRIDIKSCYDRI	99	YLQKVGIPQGSILSSFLCHFYM
eaTRT	10	GKLRLIPKKTT	0	FRPIM	67	PKLFFATMDIEKCYDSV	117	YKQTKGIPQGLCVSSILSSFYY
scTRT	13	SKMRIIPKKSN	2	FRIIA	68	PELYFMKFDVKSCYDSI	85	YIREDGLFQGSSLSAPIVDLVY
RT con		p hh h K		hR h		h hDh AF h		hPQG pP hh h
						GY		

FIG. 57B

Telomerase RT Motifs (Palm, Primer Grip)

Motif		MOTIF C		MOTIF D		MOTIF E	
TRT con		lllrl DDfL it		g n K		w g s l	
hTRT	15	LLLRLVDDFLLVT	15	GVPEYGCVVNLRKTVV	24	WCGLLLDTRTL	192
spTRT	16	VLLRVVDDFLFIT	15	GFEKHNFSTSLEKTVI	22	FFGFSVNMRSL	176
eaTRT	24	LLMRLTDDYLLIT	15	VSRENGFKFNMKKLQT	28	WIGISIDMKTL	174
scTRT	18	LILKLADDFLIIS	15	GFQKYNAKANRDKILA	25	WKHSSTMNNFH	141
RT con		h Y DDhhh F		Gh h cK h		hLG h	

FIG. 57C

FIGURE 58 (cont.)

```
                140                                                     150
trp gly leu leu leu arg arg val gly asp asp val leu val his
TGG GGG CTG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC

                                    160
leu leu ala arg cys ala leu phe val leu val ala pro ser cys
CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC

            170                                         180
ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala
GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC

                                190
thr gln ala arg pro pro pro his ala ser gly pro arg arg arg
ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT

            200                                         210
leu gly cys glu arg ala trp asn his ser val arg glu ala gly
CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

                                220
val pro leu gly leu pro ala pro gly ala arg arg arg gly gly
GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC

            230                                         240
ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly
AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC

                                250
ala ala pro glu pro glu arg thr pro val gly gln gly ser trp
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG

            260                                         270
ala his pro gly arg thr arg gly pro ser asp arg gly phe cys
GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

                                280
val val ser pro ala arg pro ala glu glu ala thr ser leu glu
GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG
```

FIGURE 58 (cont.)

290 ... 300
gly ala leu ser gly thr arg his ser his pro ser val gly arg
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

310
gln his his ala gly pro pro ser thr ser arg pro pro arg pro
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

320 ... 330
trp asp thr pro cys pro pro val tyr ala glu thr lys his phe
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

340
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

350 ... 360
leu ser ser leu arg pro ser leu thr gly ala arg arg leu val
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

370
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

380 ... 390
arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

400
leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

410 ... 420
val leu leu lys thr his cys pro leu arg ala ala val thr pro
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA

430
ala ala gly val cys ala arg glu lys pro gln gly ser val ala
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

FIGURE 58 (cont.)

```
               440                                                    450
ala pro glu glu glu asp thr asp pro arg arg leu val gln leu
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

                                460
leu arg gln his ser ser pro trp gln val tyr gly phe val arg
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

               470                                                    480
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

                                490
his asn glu arg arg phe leu arg asn thr lys lys phe ile ser
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

               500                                                    510
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

                                520
met ser val arg asp cys ala trp leu arg arg ser pro gly val
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

               530                                                    540
gly cys val pro ala ala glu his arg leu arg glu glu ile leu
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

                                550
ala lys phe leu his trp leu met ser val tyr val val glu leu
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

               560                                                    570
leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

                                580
arg leu phe phe tyr arg pro ser val trp ser lys leu gln ser
AGG CTC TTT TTC TAC CGG CCG AGT GTC TGG AGC AAG TTG CAA AGC

               590                                                    600
ile gly ile arg gln his leu lys arg val gln leu arg glu leu
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG
```

FIGURE 5B (cont.)

610
ser glu ala glu val arg gln his arg glu ala arg pro ala leu
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620 630
leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

640
pro ile val asn met asp tyr val val gly ala arg thr phe arg
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

650 660
arg glu lys arg ala glu arg leu thr ser arg val lys ala leu
AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

670
phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu
TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

680 690
gly ala ser val leu gly leu asp asp ile his arg ala trp arg
GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

700
thr phe val leu arg val arg ala gln asp pro pro pro glu leu
ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

710 720
tyr phe val lys val asp val thr gly ala tyr asp thr ile pro
TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

730
gln asp arg leu thr glu val ile ala ser ile ile lys pro gln
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

740 750
asn thr tyr cys val arg arg tyr ala val val gln lys ala ala
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

760
his gly his val arg lys ala phe lys ser his val ser thr leu
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG

FIGURE 58 (cont.)

770 780

thr asp leu gln pro tyr met arg gln phe val ala his leu gln

ACA GAC CTC CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG

790

glu thr ser pro leu arg asp ala val val ile glu gln ser ser

GAG ACC AGC CCG CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC

800 810

ser leu asn glu ala ser ser gly leu phe asp val phe leu arg

TCC CTG AAT GAG GCC AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC

820

phe met cys his his ala val arg ile arg gly lys ser tyr val

TTC ATG TGC CAC CAC GCC GTG CGC ATC AGG GGC AAG TCC TAC GTC

830 840

gln cys gln gly ile pro gln gly ser ile leu ser thr leu leu

CAG TGC CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC

850

cys ser leu cys tyr gly asp met glu asn lys leu phe ala gly

TGC AGC CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG

860 870

ile arg arg asp gly leu leu leu arg leu val asp asp phe leu

ATT CGG CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG

880

leu val thr pro his leu thr his ala lys thr phe leu arg thr

TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC

890 900

leu val arg gly val pro glu tyr gly cys val val asn leu arg

CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG

910

lys thr val val asn phe pro val glu asp glu ala leu gly gly

AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC

920 930

thr ala phe val gln met pro ala his gly leu phe pro trp cys

ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC

FIGURE 5B (cont.)

940
gly leu leu leu asp thr arg thr leu glu val gln ser asp tyr
GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC

950 960
ser ser tyr ala arg thr ser ile arg ala ser val thr phe asn
TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT GTC ACC TTC AAC

970
arg gly phe lys ala gly arg asn met arg arg lys leu phe gly
CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG

980 990
val leu arg leu lys cys his ser leu phe leu asp leu gln val
GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG

1000
asn ser leu gln thr val cys thr asn ile tyr lys ile leu leu
AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG

1010 1020
leu gln ala tyr arg phe his ala cys val leu gln leu pro phe
CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT

1030
his gln gln val trp lys asn pro thr phe phe leu arg val ile
CAT CAG CAA GTT TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC

1040 1050
ser asp thr ala ser leu cys tyr ser ile leu lys ala lys asn
TCT GAC ACG GCC TCC CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC

1060
ala gly met ser leu gly ala lys gly ala ala gly pro leu pro
GCA GGG ATG TCG CTG GGG GCC AAG GGC GCC GCC GGC CCT CTG CCC

1070 1080
ser glu ala val gln trp leu cys his gln ala phe leu leu lys
TCC GAG GCC GTG CAG TGG CTG TGC CAC CAA GCA TTC CTG CTC AAG

1090
leu thr arg his arg val thr tyr val pro leu leu gly ser leu
CTG ACT CGA CAC CGT GTC ACC TAC GTG CCA CTC CTG GGG TCA CTC

FIGURE 58 (cont.)

```
                1100                                                      1110
arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr
AGG ACA GCC CAG ACG CAG CTG AGT CGG AAG CTC CCG GGG ACG ACG

                                    1120
leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp
CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG GCA CTG CCC TCA GAC

                1130    1132
phe lys thr ile leu asp OP
TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCCACAGCCAGGCCGAGAGCAGA

CACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCCACACCC

AGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCC

GGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTC

CAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAG

CTTTTCYTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATT

CGCCATTGTTCACCCYTCGCCCTGCCYTCCTTTGCCTTCCACCCCCACCATCCAGGTGGA

GACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTA

CACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGAGGTGC

TGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGRAAAAAAAAAAAAAAAA

AAAAAAAAA
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(figure 60, SEQ ID NO:124; page 2 of 2)

1951 AGGCCCAGCATTTCACCCAGCGTCTCAAGACTCTCTTCAGCATGCTCAAC
2001 TATGAGCCGACAAAACATCCTCACCTTATGGGGTCTTCTGTACTGGGTAT
2051 GAATGACATCTACAGGACCTGGCGGGCCTTTGTGCTGCGTGTGCGTGCTC
2101 TGGACCANACACCANGATGTACTTTGTTAAGGCAGATGTGACCGGGGCCT
2151 ATGATGCCATCCCCAGGGTAAGCTGGGTGNNNNNNNNNNNNNNNNNNNNN
2201 NNNNNNNNNNNNNNNNNNNNTGGTGGAGGTTGTTGCCAATATGATCAGGC
2251 ATTCGGAGAGCACGTACTGTATCCGCCAGTATGCAGTGGTCCGGAGAGAT
2301 AGCCAAGGCCAAGTCCACAAGTCNTTTAGGAGACAGGTCACCACCTTCTC
2351 TGACTTCCAGCCATACATGGGCCAGTTCCTTAAGCATCTGCAGGATTCAG
2401 ATGCCAGTGCACTGAGGAACTCCGTTGTCATCGAGCAGAGCATCTCTATG
2451 AATGAGAGCAGCAGCAGCCTGTTTGATTCTTCCTGCACTTCCTGCGTCAC
2501 AGTGTCGTAAAGATTGGTGACAGGTGCTATACGCAGTGCCAGGGCATCCC
2551 CCAGGGCTCCAGCCTATCCACCCTGCTCTGCAGTCTGTGTTTCGGAGACA
2601 TGGAGAACAAGCTGTTTGCTGAGGTGCAGCGGGATGGGTTGCTTTTACGT
2651 TTTGTTGATGACTTTCTGTTGGTGACGCCTCACTTGGACCAAGCAXXXXX
2701 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
2751 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
2801 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
2851 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXCTGCAGTTAT
2901 GCCCAGACCTCAATTAAGACGAGCCTCACCTTCCAGAGTGTCTTCAAAGC
2951 TGGGAAGACCATGCGGAACAAGCTCCTGTCGGTCTTGCGGTTGAAGTGTC
3001 ACGGTCTATTTCTAGACTTGCAGGT

SEQ ID NO:122/123: (page 2 of 7 for Fig. 59: SEQ ID NO:122/123)

140 150
trp gly leu leu leu arg arg val gly asp asp val leu val his
TGG GGG CTG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC

160
leu leu ala arg cys ala leu phe val leu val ala pro ser cys
CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC

170 180
ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala
GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC

190
thr gln ala arg pro pro pro his ala ser gly pro arg arg arg
ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT

200 210
leu gly cys glu arg ala trp asn his ser val arg glu ala gly
CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

220
val pro leu gly leu pro ala pro gly ala arg arg arg gly gly
GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC

230 240
ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly
AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC

250
ala ala pro glu pro glu arg thr pro val gly gln gly ser trp
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG

260 270
ala his pro gly arg thr arg gly pro ser asp arg gly phe cys
GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

280
val val ser pro ala arg pro ala glu glu ala thr ser leu glu
GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG

SEQ ID NO:122/123: (page 3 of 7 for Fig. 59: SEQ ID NO:122/123)

290 300
gly ala leu ser gly thr arg his ser his pro ser val gly arg
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

310
gln his his ala gly pro pro ser thr ser arg pro pro arg pro
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

320 330
trp asp thr pro cys pro pro val tyr ala glu thr lys his phe
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

340
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

350 360
leu ser ser leu arg pro ser leu thr gly ala arg arg leu val
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

370
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

380 390
arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

400
leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

410 420
val leu leu lys thr his cys pro leu arg ala ala val thr pro
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA

430
ala ala gly val cys ala arg glu lys pro gln gly ser val ala
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

SEQ ID NO:122/123: (page 4 of 7 for Fig. 59: SEQ ID NO:122/123)

440 450
ala pro glu glu glu asp thr asp pro arg arg leu val gln leu
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

460
leu arg gln his ser ser pro trp gln val tyr gly phe val arg
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

470 480
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

490
his asn glu arg arg phe leu arg asn thr lys lys phe ile ser
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

500 510
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

520
met ser val arg asp cys ala trp leu arg arg ser pro gly val
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

530 540
gly cys val pro ala ala glu his arg leu arg glu glu ile leu
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

550
ala lys phe leu his trp leu met ser val tyr val val glu leu
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

560 570
leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

580
arg leu phe phe tyr arg lys ser val trp ser lys leu gln ser
AGG CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC

SEQ ID NO:122/123: (page 5 of 7 for Fig. 59: SEQ ID NO:122/123)

590 600
ile gly ile arg gln his leu lys arg val gln leu arg glu leu
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

610
ser glu ala glu val arg gln his arg glu ala arg pro ala leu
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620 630
leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

640
pro ile val asn met asp tyr val val gly ala arg thr phe arg
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

650 660
arg glu lys arg ala glu arg leu thr ser arg val lys ala leu
AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

670
phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu
TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

680 690
gly ala ser val leu gly leu asp asp ile his arg ala trp arg
GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

700
thr phe val leu arg val arg ala gln asp pro pro pro glu leu
ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

710 720
tyr phe val lys val asp val thr gly ala tyr asp thr ile pro
TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

730
gln asp arg leu thr glu val ile ala ser ile ile lys pro gln
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

SEQ ID NO:122/123: (page 6 of 7 for Fig. 59: SEQ ID NO:122/123)

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        740                    750
asn thr tyr cys val arg arg tyr ala val val gln lys ala ala
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

                    760
his gly his val arg lys ala phe lys ser his val leu arg pro
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC CTA CGT CCA

        770                    780
val pro gly asp pro ala gly leu his pro leu his ala ala leu
GTG CCA GGG GAT CCC GCA GGG CTC CAT CCT CTC CAC GCT GCT CTG

                    790
gln pro val leu arg arg his gly glu gln ala val cys gly asp
CAG CCT GTG CTA CGG CGA CAT GGA GAA CAA GCT GTT TGC GGG GAT

        800              807
ser ala gly arg ala ala pro ala phe gly gly OP
TCG GCG GGA CGG GCT GCT CCT GCG TTT GGT GGA TGA

TTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGT
CCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTGCGGAAGACAGTGGTGAACTT
CCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGG
CCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGA
CTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTT
CAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTC
ACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCT
ACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCAT
TTCATCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGG
CCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCA
AGGGCGCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCA
TTCCTGCTCAAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTC
AGGACAGCCCAGACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCT
GGAGGCCGCAGCCAACCCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTGAT
GGCCACCCGCCCACAGCCAGGCCGAGAGCAGACACCAGCAGCCCTGTCACGCCGGG
CTCTACGTCCCAGGGAGGGAGGGGCGGCCCACACCCAGGCCCGCACCGCTGGGAGT
CTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGT
CCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCC
GTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAGCTTTTCCTCA
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SEQ ID NO:122/123: (page 7 of 7 for Fig. 59: SEQ ID NO:122/123)

CCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATTCGCCATT
GTTCACCCCTCGCCCTGCCCTCCTTTGCCTTCCACCCCCACCATCCAGGTGGAGACCC
TGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTAC
ACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGG
TGCTGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAA

Translated Mol. Weight = 90239.69